

PD 04-MAY-2000.
 XX 28-OCT-1999; 99NC-CA00992.
 PF 28-OCT-1998; 98US-0106034.
 XX 28-OCT-1998; 98US-0106039.
 PR 28-OCT-1998; 98US-0106042.
 PR 28-OCT-1998; 98US-0106044.
 PR 28-OCT-1998; 98US-0106072.
 PR 28-OCT-1998; 98US-0106073.
 PR 28-OCT-1998; 98US-0106074.
 PR 28-OCT-1998; 98US-0106087.
 PR 02-NOV-1998; 98US-0106587.
 PR 02-NOV-1998; 98US-0106588.
 PR 02-NOV-1998; 98US-0107034.
 PR 02-NOV-1998; 98US-0107035.
 XX (CONN-) CONNAUGHT LAB LTD.
 XX Mordin AD, Oomen RP, Wang J;
 PI WPI, 2000-350688/30.
 DR P-PSDB; AAY92818.
 XX Chlamydia antigens and the proteins they encode, useful for
 PT vaccinating against Chlamydia infections that affect the respiratory
 tract
 Claim 2; Fig 1; 226bp; English.
 XX The nucleic acids may be used for the recombinant production of the
 CC Chlamydia polypeptides (either in vivo or in vitro) according to standard
 CC recombinant DNA methodologies. The polypeptides may then be used to
 CC vaccinate against Chlamydia infections in mammals. Chlamydia, such as
 CC C. pneumoniae, are pathogens responsible for upper respiratory tract
 CC infections such as community acquired pneumonia, acute respiratory
 CC disease and bronchitis and may be implicated in atherosclerotic changes
 CC and asthma. The nucleic acids may also be used as probes for detecting
 CC the presence of Chlamydia nucleic acids in samples (and therefore
 CC diagnose infections) and the proteins may be used as antigens for the
 CC production of antibodies that may be used to detect Chlamydia proteins
 CC in samples (e.g. via enzyme linked immunosorbent assay (ELISA)).
 XX Sequence 2526 BP; 693 A; 493 C; 601 G; 739 T; 0 other;
 Alignment Scores:
 Pred. No.: 3,126-315 Length: 2526
 Score: 4295.00 Matches: 841
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 21 Gaps: 0
 US-09-830-446-27 (1-841) x AAA28691 (1-2526)

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 QY
 DB 101 PheSerAsn11LeaPalaThrThrAlaSerGlyAlaAla11GlySerGluAlaAlaAsn 120
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 QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuSerProAlaSerThr 140
 DB 361 MAGACGTCACTTATCAGGATTTTCCGACCTTTCTTTCTTAATCCCGACAGATGACA 420
 QY 141 ValThrAsnGlyLeuGlyAla11LeaVal11GlyGlyAsnLeuSerLeuLeuAspAsp 160
 DB 421 GTGACTTAATGATTTGGAGCTATCAATGTTAAAGGAATTAAGCTTAATGATTAATGAT 480
 QY 161 LysValLeu11GlnAspAsnPheSerThrGlyAspGlyVal11LeaVal11LeaVal11Gly 180
 DB 481 AAGTATTGATTCAGACCAATTTCTCAACAGGAGAGGCGGACCAATTAATGTCAGGC 540
 QY 181 SerLeu11Lea11AsnAsn11LeuSerLeuSerPhe11GlyAsnSerSerThrArg 200
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 DB 661 GGGAAATACAGCGCTACCGCTGCTGTAAAGGAGGCTATCCGATTCAGACTGCTGCG 720
 QY 241 ThrLeuSer11LeuSerGlyAspSerGlyAsp11LeaPheGluGlyAsnThr11GlyAla 260
 DB 721 ACCCTTAATCAATTTCTGAGACAGTGGGACATTAATTTTGAAGGCAATACGATGAGAGCT 780
 QY 261 ThrGlyThrValSer11LeaSerAla11LeaPheGlyThrSerAlaLys11LeaThrAlaLeu 280
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 QY 301 SerVal11AspAlaLeuSer11LeaSerProAspThrGlyAspAsn11GlyGlyThr 320
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 QY 601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
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 QY 621 LeuTyrSerValValSerIleLeuLeuGlyGlnGlyLysLeuArgGlnIleLeuLeuPro 640
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 QY 641 TyrValSerIleuSerProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
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 QY 761 HisValValAlaMetTyrSerProAspValCysArgSerAsnProLysCysThrThrThr 780
 Db 2281 CATGTTTACGATGATTTCTCCAGATGTTTGTCTGTAAGTAAACCCCAATATGACACTACC 2340
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 QY 801 IleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAlaGlnLeuPheGlyAsnPhe 820
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QY 821 GlyPheGlnThrArgGlySerSerArgSerTyrAsnValAspAlaGlySerLysIleLys 840
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 RESULT 2
 ABL91253 standard; DNA; 2526 BP.
 ID ABL91253
 AC ABL91253;
 DT 29-JUL-2002 (first entry)
 XX
 DE Chlamydia pneumoniae cp6270 ORF DNA, SEQ ID NO:140.
 XX
 KW Chlamydial infection; antigen; immunogen; vaccine; diagnosis;
 KW human respiratory disease; cardiovascular disease; atherosclerosis;
 KW coronary artery disease; carotid artery stenosis; myocardial infarction;
 KW cerebrovascular disease; aortic aneurysm; claudication; stroke;
 KW strain CWL029; open reading frame; ORF; gene; ds.
 XX
 OS Chlamydia pneumoniae.
 XX
 FH Key
 FT Location/Qualifiers
 FT CDS
 FT 1..2526
 FT /tag= a
 FT /product= "cp6270"
 FT sig_peptide
 FT 1..54
 FT /tag= b
 FT mat_peptide
 FT 55..2523
 FT /tag= c
 FT /product= "Mature protein"
 PN
 XX
 PD 10-JAN-2002.
 XX
 PF 03-JUL-2001; 2001WO-1B01445.
 PR 03-JUL-2000; 2000GB-0016363.
 PR 11-JUL-2000; 2000GB-0017047.
 PR 21-JUL-2000; 2000GB-0017983.
 PR 07-AUG-2000; 2000GB-0019348.
 PR 18-AUG-2000; 2000GB-0020440.
 PR 14-SEP-2000; 2000GB-0022583.
 PR 10-NOV-2000; 2000GB-0027549.
 PR 22-DEC-2000; 2000GB-0031706.
 XX
 PA (CHIR-) CHIRON SPA.
 XX
 PI Rattl G, Grandi G;
 XX
 DR WPI; 2002-154726/20.
 DR N-PSDB; ABB90595.
 XX
 PT Novel Chlamydia pneumoniae protein useful in the manufacture of a
 PT medicament for treatment or prevention of infection due to Chlamydia,
 PT preferably Chlamydia pneumoniae, and for diagnostic purposes
 XX
 PS Claim 5; Page 110-111, 364pp; English.
 CC
 CC Sequences ABB90526-ABB90715 represent novel proteins from Chlamydia
 CC pneumoniae (strain CWL029), and ABL91184-ABL91373 represent DNA encoding
 CC them. The proteins are predicted to be immunogenic and may therefore be
 CC useful in vaccine production and for diagnostic purposes. Chlamydia
 CC pneumoniae is a common cause of respiratory disease in humans, and is
 CC also involved in the development of cardiovascular diseases such as
 CC atherosclerosis, coronary artery disease, carotid artery stenosis,
 CC myocardial infarction, cerebrovascular disease, aortic aneurysm,
 CC claudication and stroke. The proteins and nucleic acids of the invention

CC may be used in vaccines and pharmaceutical compositions for the
 CC prevention or treatment of chlamydial infections, particularly Chlamydia
 CC pneumoniae infections. The proteins may also be used in the detection of
 CC Chlamydia pneumoniae, and the nucleic acids may be used in PCR, branched
 CC DNA probe assay or blotting techniques for determining Chlamydia
 CC pneumoniae gene expression. The present sequence represents a
 CC specifically claimed DNA which encodes a Chlamydia pneumoniae protein of
 CC the invention.

XX Sequence 2526 BP; 693 A; 493 C; 601 G; 739 T; 0 other;

Alignment Scores:

Pred. No.:	3,12e-315	Length:	2526
Score:	4295.00	Matches:	841
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	24	Gaps:	0

US-09-830-446-27 (1-841) x ABL91253 (1-2526)

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QY 21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
DB 61 TTATTAGAGCGCTGCTACTACCGAAGGTTATCGCTACGCAATAGCTTCATGGAATCTACA 120
QY 41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnTyraPhe 60
DB 121 TCAACACACAGCTTTCTAGTAAACATCATCGCTACAGATGGACCAATTAATGTTTTT 180
QY 61 LysAspSerValValIleGluLeuAsnValProLysThrGlyIleThrGlnSerThrSerCys 80
DB 181 AAGAGATTCTGTAGTATAGAAAAATGTAACCAAAACAGGGGAAACCTCAGTCTAGTTGT 240
QY 81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
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QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlyAlaAlaAsn 120
DB 301 TTTAGCAATATCGATCAACACAGGCTTCGAGCTGCTATTGGAAGTGAAGAGCTTAAT 360
QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
DB 361 AAGACAGTCACGTTATCAGGATTTTCGGCACTTTCTTTCTTAAATCCCCACACAGTTACA 420
QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAsp 160
DB 421 GTGACTAAATGCAATGGAGCTACTCAATGTTAAAGGAAATTTAAGCTTATGGAATTAAT 480
QY 161 LysValLeuIleGluAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
DB 481 AAGGATTAATGATTCAGGCAATTTCTCAACAGGAGAGTGGGAGCAATTAATTTGTGAGGC 540
QY 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
DB 541 TCCCTTGAAATCGCAAAACAATAGTCCCTTTCTTTATTTAGAAATGTTCTTCAACACCT 600
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QY 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
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QY 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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QY 281 ArgAlaAlaGlnGlyHisThrIleTyThrPheTyraAspProIleThrValThrGlySerThr 300
DB 841 CGTGTGGGCAAGGACATACATATACCTTTATGATGTCGAATTAAGTAAACAGATCGACA 900
QY 301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlyThrThr 320
DB 901 TCTGTGCTGATGCTCTCATATTAATATAGCCCTGATCTGAGATATACAAAGATATACG 960
QY 321 GlyThrIleValPheSerGlyGlyLysLeuThrGluAlaGluAlaLysAspGlyLysAsn 340
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DB 1141 TTAGGAGAGTGTGTTGTTGCAAAACCGAAAGTATCGAGTTAAGCAATTTGGAATTAAT 1200
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QY 481 LysTrpThrIleAsnTrpSerThrAspAspLysValAlaThrValSerTrpAlaLysGln 500
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 QY 641 TyrrValSerLysThrLeuProCysSerPheTyrrGlyIleLeuSerTyrrHisThrAsp 660
 DB 2021 TATGTTCCAGACTCTGCTGCTCTTTCTATAGGACAGCTTACCTAGCGCATACGAT 2080
 QY 661 HisArgMetLysThrGlySerLeuProProProProProProProProProProProPro 680
 DB 2081 CATGCAAGAGACCGAGCTCTACCCCCCCCCCCCCCGAGCTCTCGACGATCATACT 2140
 QY 681 SerTrpGlyGlyTyrrValTrpAlaGlyGlyLeuGlyThrArgValAlaValGlyLysThr 700
 DB 2141 TCTTGGGAGATATGCTGCGGCTGAGAGCTGGAGACCTCGATGCTGTGAAATATCC 2200
 QY 701 SerGlyArgGlyPhePheGlnGlyTyrrThrProPheValLysValGlnAlaValTyrrAla 720
 DB 2201 ACGGCAAGATTTTCCAGAGATCACTCCATTTGTAAGTCCAGACTTTTACGCT 2260
 QY 721 ArgGlnAspSerPheValGlyLeuGlyValAlaIleSerArgAspPheSerAspSerHisLeu 740
 DB 2261 CGCCAAAGATAGCTTGTGAACCTAGAGCTATCACTCGATTTTATGATTCGATCTT 2320
 QY 741 TyrrAsnLeuAlaIleProLeuGlyIleLysLeuGlyLysArgPheAlaGlyGlnTyrr 760
 DB 2321 TATAACTCTGCAATCTCTTGGAAATCAAGTTAGAAACGCTTTGCGAGAGCAATATAT 2380
 QY 761 HisValValAlaMetTyrrSerProAspValCysArgSerAsnProLysCysThrThrThr 780
 DB 2381 CATGTTGATGATATTTCTCAGATGTTGCTAGTAATCCCAATATGATGATGATGATGAT 2440
 QY 781 LeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAlaGly 800
 DB 2441 CTACTTTCACCAAGGAGGTTGAAAGCAAAAGTTTGAACCTTGAAGACAGAGCTGCT 2500
 QY 801 IleValGlnAlaSerGlyPheArgSerLeuGlyValAlaAlaGlyLeuPheGlyAsnPhe 820
 DB 2501 ATTTGTCAGGCTCAGGTTTGTGATCTTTGGAGCTGAGCAGACCTTTCCGGAACTTT 2560
 QY 821 GlyPheGlyTrpArgGlySerSerArgSerTyrrAsnValAspAlaGlySerLysIleLys 840
 DB 2561 GCTTGAATGCGGGATTTCTCTGATGATATGATGATGATGATGATGATGATGATGAT 2620
 QY 841 Phe 841

DB 2621 TTT 2623

RESULT 4
AA06819
ID AAX06819 standard; DNA; 2526 BP.
XX

AC AAX06819;
XX
DT 26-APR-1999 (first entry)
XX

Chlamydia pneumoniae surface exposed protein Omp7 DNA.
XX
OM7; outer membrane protein 7; surface exposed protein; antigen;
KW infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX
OS Chlamydia pneumoniae.
XX
PN W09658953-A2.
XX
PD 30-DEC-1998.
XX
PF 19-JUN-1998; 98MO-DK00266.
XX
PR 23-JUN-1997; 97DK-0000744.
XX

(BIRK/) BIRKELUND S.
PA (CHRI/) CHRISTIANSEN G.
XX
XX Birkelund S, Christiansen G, Knudsen K, Madsen A;
PI Mylund P;
XX
XX WPI; 1999-105610/09.
DR P-PSDB; AAW88420.
XX

Species-specific test for identifying mammals infected with
PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins

Claim 6; Page 49-50; 115pp; English.

This DNA sequence codes for the novel 89.7 kDa surface exposed
CC protein Omp7 (see AAW88420) of the human respiratory pathogen
CC Chlamydia pneumoniae. By generating antibodies against C.
CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
CC was obtained which reacted with outer membrane proteins. The
CC antibody was used to identify the genes (see AAX06816-27) encoding
CC Omp4-Omp15 proteins (see AAW88417-28) in an expression library of
CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
CC Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
CC the other, and encode polypeptides of about 89.6-100.3 kDa and
CC about 56.1 kDa. The invention provides a new species specific test
CC for identifying mammals (including humans) infected with Chlamydia
CC pneumoniae. The test comprises detecting antibodies specific for
CC Omp4-Omp15 or detecting nucleic acid fragments encoding these outer
CC membrane proteins, especially by PCR. The proteins are also used
CC in the diagnosis of C. pneumoniae infection in mammals. The
CC nucleic acids and proteins can also be used in the immunisation of
CC mammals, the nucleic acids being particularly useful as DNA
CC vaccines for effecting in vivo expression of antigens. The
CC vaccines may also prevent atherosclerosis and bronchial asthma,
CC which are possibly associated with C. pneumoniae.
XX

Sequence 2526 BP; 696 A; 495 C; 597 G; 738 T; 0 other;
SQ

Alignment Scores:
Pred. No.: 6, 04e-314 Length: 2526
Score: 4278.00 Matches: 837
Percent Similarity: 99.888 Conservative: 3
Best Local Similarity: 99.528 Mismatches: 1
Query Match: 99.608 Indels: 0
DB: 20 Gaps: 0

US-09-830-446-27 (1-841) x AAX06819 (1-2526)

QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAen 20
DB 1 ATGAAGATTCCACCTCCGCTTTTATTGATATCATTAAGTACCACTTCTCATATGTCGAAT 60

QY 21 LeuLeuGlyAlaAlaThrThrGluLeuSerAlaSerAenSerPheAspGlyThrThr 40
DB 61 TTATTAGAGAGCTGCTACTACCGAAGAGCTATCGCTACCAATAGCTGATGGAAGTACA 120

QY 41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnYrAlaPhe 60
DB 121 TCAACAAACAGCTTTTTCAGTAAACATCTCGCTACAGATGAGCAACCAATTATTTT 180

QY 61 LysAspSerValValIleGluAsnValProLysThrGlyLysThrGlnSerThrSerCys 80
DB 181 AAGATTCTGTAGTATTAGAAAATGTACCAAAACAGGGAAACTGACTCTAGTTGT 240

QY 81 PheLysAsnAspAlaAlaGlyAspLeuAsnPheLeuGlyGlyLysPheSerPheThr 100
DB 241 TTTAAATAATGACGCTGACGCTGAGATCTAAATTTCTTAGAGGGGGAATTTCTTTCACA 300

QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
DB 301 TTACCAATATCGATGCAACCAACGCTTCTGAGCTGCTATTGGAAGTGAACACACTAAT 360

QY 121 LysThrValIleThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
DB 361 AAGACAGTCACGTTATACGAGATTTTGGACCTTCTTTTAAATCCCAACCAAGTACA 420

QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuAspAsnAsp 160
DB 421 GTGACTAATGATGAGTGGAGCTATCAATGTTAAAGGAATTATAGCTATGATATGAT 480

QY 161 LysValIleuIleGluAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
DB 481 AAGGATTGATTTCAGACAAATTTCTCAACAGAGATGCGGAGCAATTATTTGTCCAGGC 540

QY 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
DB 541 TCTTGAAAGATCGCAACAAATATAGTCCCTTCTTTATTTGAAATAGTTCTTCAACACT 600

QY 201 GlyGlyAlaIleHisThrLysAsnLeuThrLysSerSerGlyGlyGluThrLeuPheGln 220
DB 601 GCGGAGGAGATTCAATACCAAAACTCAACATGTTCTGGTGGGAACTATTTACG 660

QY 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyAlaIleAlaIleAlaAspSerGly 240
DB 661 GGGATACAGCGCTACGCGCTGCTGTAAAGAGGTGCTATCGCATTCGACACTCTGGC 720

QY 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
DB 721 ACCCTATTCATTTCTGGAGACAGTGGCAATTAATCTTTGAAAGCAATACGATAGAGCT 780

QY 261 ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeu 280
DB 781 ACGAGAACCGTCTCTCATAGTCTATTTAGTAAGAACTAAGCGCTAAGATACTCGTTA 840

QY 281 ArgAlaAlaGlnGlyHisThrIleThrPheThrAspProIleThrValThrGlySerThr 300
DB 841 CGTGTGCGCAAGACATACGATATATCTTTATGATTCGATACGTAACAGATCGACA 900

QY 301 SerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGluYrThr 320
DB 901 TCTGTGCTGATGCTCTCAATATTAATAGCCCTGATACGAGATACAAAGATATCG 960

QY 321 GlyThrIleValPheSerGlyLysLeuThrGluAlaGluAlaLysAspGlyLysAsn 340
DB 961 GGAACCATATGCTTTTCTGAGAGAACTCAACGAGGCAAGAGCTAAGATGAAGAAGAC 1020

QY 341 ArgThrSerLysLeuLeuGluAsnValAlaPheLysAsnGlyThrValValLeuLysGly 360

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Db      1021 CGCAGCTCTAAATTAATCTCAAAATGTGCTTTTAAAAATGGGAGCTAGTATTTAAAGCT 1080
Qy      361  ASPPVALLIIEUSERRLAANGIYPHESERGINAPRALAASERLYLEULILEMETAP 380
Db      1081 GATGTCGTTTAAAGCGAAACGGTTTCTCTCAGAGTCAACCTTAAGTATTAATGAT 1140
Qy      381  LEUGLYTHSERLEUVALAALAAANTHGIUSERILEGLUEUTHASMLEUGIULLEAN 400
Db      1141 TTAGGACCTGCTTGTTGGTCCAAACACCGAAATATCGAGTTACCAATTTGGAATTAT 1200
Qy      401  ILEAPSERLEUARGANGIYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLYLY 420
Db      1201 ATAGACTCTCTCAGAGACCGGAAAAAGATAAACTCAGTGGCCAGCTCAGAAAGAT 1260
Qy      421  ILEAGGIIIEAPARGPROVALIILEUVALIIESEAPSGIUSERPHETRYGIDANGIY 440
Db      1261 ATTCGTATAGATCGCTCGTGTGTACTGGCAATTAGGATGAGATTTTATCAAAATGCG 1320
Qy      441  PHELEUAENGILUAPHISERTYRAPHGIYILEUGLULEUAPRALAGIYLYSAPRIIE 460
Db      1321 TTTTGGATGAGACCAATTCCTATGATGGGATTTCTTGAGTTAGATGCTGGGAAACATC 1380
Qy      461  VALIIESERALAASERARGSERIIEAPRALAVALGINSEPROTYGITYGIDANGIY 480
Db      1381 GGATTTTTCGACGATTTCTCGAGTATAAATGCTGTACATCTCCGATGGCTATCAGGGA 1440
Qy      481  LYETTPTRHIIIEANTTPSERTHRAPAPLYELYBALATHVALISERTPALALYSGIN 500
Db      1441 AAGTGACACATCAATGATGCTACTAGATGATGATGATGATGATGATGATGATGATG 1500
Qy      501  SERPHEAENPROTHRALAGIUGINGIUALAPROLEUVALIIESEAPSGIUSER 520
Db      1501 AGTTTAAATCCCACTGCTGAGAGAGAGGCTCCGTTAGTTCTTAATCTTTGGGGTTCT 1560
Qy      521  PHEIIEAPVALIARGSERPHEGINAPHEIIEGLULEUGIYTHGIDANGIYLAAPROY 540
Db      1561 TTTATATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 1620
Qy      541  GIULYVARGPHEPTRVALIAGIYIIESEAPVALIIEHIAARGSERIYVARGIULAN 560
Db      1621 GAAAGAGATTTTGGGTTGAGGCAATTTCCAAATGTTTGCATAGAGACCGGTGTAAGAT 1680
Qy      561  GINARGLYPHEARGHISVALISERGIDYALAVAIAGIYALASERTHARGHECTPRO 580
Db      1681 CAAGGAAATTCGCTCATATGATGAGGAGGCTGCTGATGATGATGATGATGATGATG 1740
Qy      581  GIYGIYAPPTHRLEUSERLEUGIYPHEALAGIULEUPHEALARGAPLYAPPTYPHE 600
Db      1741 GGTGGGATACCTTGCTGCTGGGTTTGTCTCAGCTCTTTGGCGGTGACAAAGACTACTT 1800
Qy      601  METAENTHRAHPHEALALYETHRTYRALAGIYSELEUARGLEUGIINHIAAPLASER 620
Db      1801 ATGAATTAACCAATTTCCCAAGACCTTAAGCAGATCTTTACGTTTGACAGACATGCTTC 1860
Qy      621  LEUYSERSEVALISERILEULEUGIYGLUGIYGLIYLEUARGIULILEULEUPRO 640
Db      1861 CTATACTCTGCTGTGATGATCTCTTTTGAAGAGAGGAGACCTCCGCAATCTCTGTTGCT 1920
Qy      641  TYRVALISERLYSETHLEUPROCYSESPHEIYRGIDYGLIYSELEUARGIYHISHTHAP 660
Db      1921 TATGTTTCCAAAGCTGCGCGTGTCTTTCTATGGCAGCTTATGATGATGATGATGATG 1980
Qy      661  HISARGMETLYSETHGIUSERLEUPROPROPROPROPROTHLEUSERTHRAPHSHTH 680
Db      1981 CATCGATTAAGACCAAGCTCTACACCCGCCGCCGCCGCCGCCGCCGCCGCCGCCGCC 2040
Qy      681  SETTRIGIYGLIYTYRVALITPALAGIYGLIYGLIYGLIYGLIYGLIYGLIYGLIY 700
Db      2041 TCTTGGGAGAGATATGCTGCTGGGAGAGCTGGGAATCGAATCTGTTGAAAATACC 2100
Qy      701  SERGIYARGIYYPHEPHEGINIYTYRTHRPHOPEVALIYVAGIULIYVALIYTRALA 720
Db      2101 AGCGGAGAGAGATTTTCCAGAGATACACTCACTTTGTAAGTCCAAAGCTGTTTACTCG 2160

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Qy      721  ARGGINAPSERPHEVALIGIULEUGIYVALIIESEARARGAPPHESERAPSERHISLEU 740
Db      2161 CGCCAGATAGACTTTGTTGAACCTAGAGCTATCATGATGATTTTATGATTCGCATCTT 2220
Qy      741  TYRANLEUALAIIIEPROLEUGIYIIEYSELEUGIULYVARGPHEALAGIULITTYR 760
Db      2221 TATAACTTGCGATTCCTCTTGGAAATCAAGTTAGAGAAACGGTTTGGCAGACCAATATTAT 2280
Qy      761  HISVALIYALAMETRYSERPROAPVALIYVARGSERAPPOLYSCYETHRTHR 780
Db      2281 CATGTGTAGGAGATGATTTCTCCAGATGTTGTGTGATGAACCCCAATGTACACATACC 2340
Qy      781  LEUUSERAENGINGIYSETRIPLYETHRILYSGIYSEANLEUALAARGIYALAGIY 800
Db      2341 CTACTTTCCAAACCAAGGAGTGGTAAGACCAAGGTTGAACTTAGCAAGACAGCTGCT 2400
Qy      801  ILEVALGINALASERGYPHEARGSERLEUGIYALALAGIULEUPHEGIYASNPHE 820
Db      2401 ATGTTCAGGCTCAGGTTTTCGATCTTTGGGAGCTGCAGACAGACTTTTCGGGAACTTT 2460
Qy      821  GLYPHEGIUTPALGGLYSESERARGSETRYRANVALIAPRALAGIYSEIYHILEYS 840
Db      2461 GGCCTTGAAATGCGCGGATCTTCTGTAATGATGATGATGATGATGATGATGATGATG 2520
Qy      841  PHE 841
Db      2521 TTT 2523

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RESULT 5

AA91990 standard; DNA; 1230025 BP.

AA91990;

13-SEP-1999 (first entry)

Nucleotide sequence of the complete genome of *Chlamydia pneumoniae*.

Respiratory disease; pneumonia; bronchitis; heart disease; sarcoidosis;

sinusitis; purulent otitis media; erythema nodosum; pharyngitis;

vaccine; neutralising epitope; ss.

Chlamydia pneumoniae.

MO9927105-A2.

03-JUN-1999.

20-NOV-1998; 98MO-IB01890.

04-NOV-1998; 98US-0107078.

21-NOV-1997; 97FR-0014673.

(GENST) GENSET.

Griffais R;

WPI; 1999-357842/30.

Genome sequence of *Chlamydia pneumoniae*

Claim 1; Page 291-611; 1912pp; English.

The present sequence represents the complete genome of *Chlamydia pneumoniae*, and encodes proteins AA934584-Y35879. *C. pneumoniae* causes respiratory disease such as pneumonia and bronchitis and is thought to be a contributing factor in heart disease, sarcoidosis, sinusitis, purulent otitis media, erythema nodosum or pharyngitis. The polypeptides encoded by the open reading frames of the *C. pneumoniae* genome (see CC AA934584-Y35879) can be used in immunogenic compositions as vaccines. CC Vectors containing *C. pneumoniae* nucleotide sequences can also be used as immunogenic compositions, especially where the vector directs

CC the expression of a neutralising epitope of *C. pneumoniae*.

Sequence 1230025 BP; 367213 A; 249833 C; 249013 G; 363589 T; 377 other;

Alignment Scores:

Pred. No.:	8e-309	length:	1220025
Score:	4255.00	Matches:	840
Percent Similarity:	99.76%	Conservative:	0
Best local Similarity:	99.76%	Mismatches:	1
Query Match:	99.07%	Indels:	2
DB:	20	Gaps:	0

US-09-830-446-27 (1-841) X AAX91990 (1-1230025)

QY	28550	ATGAAAGTTCCACTCCGCTTTTATTGATATACATGATCTACGCTTCTATGTCGAAT	29009
QY	21	LeuLeuG1yAla1aThrThrG1uLeuSer1aSerAnSerPheApG1yThrThr	40
Db	29010	TTATTAGAGCTGCTACTACCGAAGAGTTATCGGCTTTCGCAATAGCTTCGATGGAAGCTACA	29069
QY	41	SeThrThrSerPheSerSerLyThrSerSerAlaThrApG1yThraAntyValPhe	60
Db	29070	TCAACAAACAAGCTTCTCTAGTAAACATCATCGGCTACAGATGGCAACCAATATGTTTT	29129
QY	61	LyApSerSerVal1a11eG1uAnSerAlaProLyThrG1yG1uThrG1nSerThrSerCyS	80
Db	29130	AAAGATTCTTGATAGTTATGAAATAATGTAACCAAAACAGGGAAACTAGTCTACTAGTTGT	29189
QY	81	PheLyApAnApAla1a1aG1yApPLeuAnPheLeuG1yG1yPheSerPheThr	100
Db	29190	TTTTAAATACACGCTGACCTGAGATCTAAATTTCTTGAAGGGGGATTTTCTTTCA	29249
QY	101	PheSerAn11eApAlaThrThrAlaSerG1yAla1a11eG1ySerC1uAlaAn	120
Db	29250	TTTTGCAATTCGATGACCAAGGCTTCGAGAGCTGATATGGAATGAAAGAGCTAAT	29309
QY	121	LyThrVal1ThrLeuSerG1yPheSerAlaLeuSerPheLeuLySerProAlaSerThr	140
Db	29310	AAGACAGTCAAGTATCAGAGATTTTGGGACTTTCTTTCTTAAATCCCAACAGTACA	29369
QY	141	Val1ThrAnG1yLeuG1yAla11eAnValLyG1yYAnLeuSerLeuLeuApAnAp	160
Db	29370	GTCATATGATGATTTGGAGCTATCAAGTTAAAGGAATTTAAGCCTATGATATATGAT	29429
QY	161	LyThrAlaLeu1eG1uAnPAnPheSerThrG1yYApG1yG1yAla11eAnCyAlaG1y	180
Db	29430	AAAGTATTTGATTCAGACCAATTTCTCAACAGAGATGGCGGACAATTAAATGTGCAAGC	29488
QY	181	SeLeuLyS11eAlaAnAnAnLySerLeuSerPhe11eG1yAnSerSerThrArg	200
Db	29489	TCCCTGGAAGATCGCAACAATTAAGTCCCTTCTTTATGGAATATGTTCTTCAACACGT	29548
QY	201	G1yG1yAla11eThrThrLySaAnLeuThrLeuSerSerG1yG1yG1uThrLeuPheG1n	220
Db	29549	GGCGAGCGATTCATACCAAAAACCTCACATCTTCGAGGGGAACTCTAATTTG	29608
QY	221	G1yAnAnThra1aProThra1a1aG1yLyG1yG1yAla11eAla11eAlaAnPheSerG1y	240
Db	29609	GGGAATACAGCGCTTACGGCTGCGTAAGAAGAGGTGCTATGCGATTCAGACTTGGC	29668
QY	241	ThrLeuSer11eSerG1yApPSeSerG1yApP11e11ePheG1uG1yAnThr11eG1yAla	260
Db	29669	ACCTCATTCATTTCTGAGACAGGGGCAATTAATCTTGAAGGCAATACGATAGAGCT	29728
QY	261	ThrG1yThrValSer11aSerAla11eApLeuG1yThrSerAlaLyS11eThra1aLeu	280
Db	29729	ACAGAAACCGTCTCTCATAGCTATGATTTTGAAGACATAGCCTTAAGATACGTGCTTA	29788
QY	281	ArgAlaAlaG1nG1yH1eThr11eTyPheTyApPPro11eThrValThrG1ySerThr	300
Db	29789	CGTCTCGGACAGACATACGATATACTTTTATGATCCGATTTCTGTAAACAGATTCACA	29848

OY	301	SeVValAlaAspAlaLeuEniLeaSenProAspThrGlyAspAsnLysGlyLysThr	320
Db	29849	TCGTGTCTATGCTCTCAATATTAAATACCCCTGATACGGAGATACAAAGATATACG	29908
OY	321	GIYThrIleValPheSerGlyGlyLysLeuThrGluAlaGlyAlaLysAspGlyLysAsn	340
Db	29909	GGAACCAATCTCTTTCTGTGAGAGAAAGCTCACAGAGCGAAGAGCTTAAGATGAAAGAC	29968
OY	341	ArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeu-LysGly	360
Db	29969	CGCACTTCCTAAATTACTTCMAAATGTTGCTTTTAAAAAGGACGTGATGTTTGAAGAGG	30028
OY	360	YAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAs	380
Db	30029	TGATGTGCTTTTAAGTCGCAAGCGTTTCTCTCAGATGCAAACTTAAGTTATATATGCA	30088
OY	380	PLeuGlyThrSerLeuValAlaAsnThrGlySerIleGlyLeuThrAsnLeuGlyIleAs	400
Db	30089	TTTAAAGGACGTCTGTGGTTGCCAAACACCGAAAGTATCGAGTTTACGAATTTGGAATTAA	30148
OY	400	nIleAspSerLeuAspAsnGlyLysLysLysLysSerAlaAlaThrAlaGlyLysAs	420
Db	30149	TATAGACTCTCTCAGAGAACGGGAAAAAGATAAACCTCACTGCTGCACAGCTCAGAAAGA	30208
OY	420	PLeuArgIleAspAspProValValLeuAlaIleSerAspGlySerPheTyGlnAsnGly	440
Db	30209	TATTGCTATGATACGTCTCTGTTGTAATGGCAATTAAGCATGAGAGATTTTATCAAAATGG	30268
OY	440	yPheLeuAsnGlnAspHisSerTyraAspGlyIleLeuGlyLeuAspAlaGlyLysAspI	460
Db	30269	CTTTTGGAAAGAGACACCATTCCTATGATGGAGATTCCTTGAGTTAGATGCTGGAAAGACAT	30328
OY	460	eValIleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyGlyTyGlnGly	480
Db	30329	CGTATTTCTGCAAGATTCCTGCAATATAGTGTCTGACAACTCCGTAATGCTATACGGG	30388
OY	480	YLYSTripThrIleAsnTripSerThrAspLysLysAlaThrValSerTripAlaLysGly	500
Db	30389	AAAGTGCACGATCAATTGGCTCTACTGATGATTAAGAAAGCTACGGTTCCTGGGCAAGCA	30448
OY	500	nSerPheAsnProThrAlaGlnGlnGlnAlaProLeuValProAsnLeuLeuTripLys	520
Db	30449	GAGTTTAAATCCACAGCTGAGAGAGAGGCTCGTAAATCTTCTTGGAGTTC	30508
OY	520	rPheIleAspValArgSerPheGlnAsnPheIleGlyLeuGlyThrGlnGlyAlaProTy	540
Db	30509	TTTTATATGAGTTCGTTCTCTCCAGAAATTTATATAGCTATAGATCTGAAGAGTCTCTTA	30568
OY	540	rGlyLysArgPheTripValAlaGlyLysSerAsnValLeuHisValArgSerGlyArgGlnAs	560
Db	30569	CGAAAGAGATTTTGGGTGGCAGAGCATTTCCAAATGTTTTGCAATAGAGCGGCTCGAAGAA	30628
OY	560	nGlnArgLysPheArgHisValSerGlyGlyAlaValAlaGlyAlaSerThrArgMetPro	580
Db	30629	TCAAGAGAAATTCGCTCATGTAGTGTAGAGGTCTGTAGTAGGTCTTACGACAGAGATGCC	30688
OY	580	OGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrePh	600
Db	30689	GGGTGGGATACCTTGCTCTCGGAGTTTCTCAAGCTCTTGCGCGGACAAAGACATCACTT	30748
OY	600	eMetAsnThrAsnPheAlaLysThrTyraLacLysSerLeuAlaGlyLeuGlnHisAspAlaSe	620
Db	30749	TATGAATACCAATTTGGCAAGCCTCACAGAGATTTTACGTTGGACAGACAGATGCTTC	30808
OY	620	rLeuTySerValValSerIleLeuLeuGlyGlyGlyIleAspArgGlyIleLeuLeuPro	640
Db	30809	CCATATATCTGTGTGTAGATATCTTTTAAAGAGAGGAGAGACCTCCGGAATCTCTGTGTC	30868
OY	640	OTYrValSerLysThrLeuProCysSerPheTyrglyGlnLeuSerTyrglyHisThrAs	660
Db	30869	TTATGTTTCCAAAGACTGCGCTGCTTTTCTATAGGCAAGCTTATAGGCAATGCGCAATACGA	30928

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QY 660 PHISARMEUlyTHrGluSerLeuProProProProThrLeuSerThrAspHisIsth 680
DB 30929 TCATGCGATGAAAGACGAGCTCTACCCCCCCCCCGAGCGCTCTGACGAGCATATAC 30988
QY 660 rSerTrpGlyGlyIYrValTTPAlAGlyGluLeuGlyThrArgValAlaValGluAsnTh 700
DB 30989 TTCCTGGGAGAGATATGCTGGGCTGAGAGCTGGGAACTCGAGTTGCTTGAATAATAC 31048
QY 760 rSerGlyArgGlyPhePheGlnGluTyrThrProPheValysValGlnAlaValTyrAl 720
DB 31049 CAGCGGACAGAGATTTTCCAAAGAGTACCTCATTTGTAAGTCCAAAGCTGTTTACGC 31108
QY 720 AArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSerAspSerHisIle 740
DB 31109 TCGCCAAAGTACCTTGTAGACTGAGACTATGCTGATTTTAGATTCGATTCGATCT 31168
QY 740 uTyrAsnLeuAlaIleProLeuGlyIYleIysLeuGluIysArgPheAlaGluGlnTyrTy 760
DB 31169 TTATTAACCTTGCATCTCTCTGGAATCAAGTTAGAAACGGTTTGCAGACCAATATTA 31228
QY 760 rHisValValAlaMetTyrSerProAspValCysArgSerAspProIysCysThrThTh 780
DB 31229 TCATGTTGAGGATGATTTCTCCAGATGTTGTGTAGTAAACCCCAATGTACCATAC 31288
QY 780 rLeuLeuSerAengGlnGlySerTrpIYrThrIYsGlySerAenLeuAlaArgGlnAlaG 800
DB 31289 CCTACTTTCCAAACCAAGGAGTTCGAAAGCCAAAGTTGAACTTTCAGCAAGCAGGCTGG 31348
QY 800 YIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaIleGluLeuPheGlyAsnPh 820
DB 31349 TATGTTACGAGCTCAGGTTTTCGATCTTGGAGAGCTGCAGACAGCTTTTCGGAATCT 31408
QY 820 eGlyPheGluTTPArgGlySerSerArgSerTyrAsnValAspAlaGlySerIYsIleY 840
DB 31409 TCGCTTGAATGCGCGGATCTTCTCGTAGTATATGATGCGCGTAGCAAAATCA 31468
QY 840 aspHe 841
DB 31469 ATTT 31472

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RESULT 6
AAx06830
ID AAX06830 standard; DNA; 1830 BP.
AC AAX06830;
XX 26-APR-1999 (first entry)
DT Chlamydia pneumoniae surface exposed protein Omp7 DNA.
DE Chlamydia pneumoniae surface exposed protein; antigen;
XX Omp7; outer membrane protein 7; surface exposed protein; antigen;
XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
XX Chlamydia pneumoniae.
OS WO9858953-A2.
XX PN 30-DEC-1998.
XX PD 19-JUN-1998; 98WO-DK00266.
XX PF 23-JUN-1997; 97DK-0000744.
XX PR (BIRK/) BIRKELUND S.
XX PA (CHRI/) CHRISTIANSEN G.
XX PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
XX PI Mygind P;
XX WPI; 1999-105610/09.
XX DR P-PSDB; AAW88431.
XX PT Species-specific test for identifying mammals infected with

```

PT Chlamydia pneumoniae - comprises detecting antibodies specific for
PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
PT these proteins
PS Disclosure; Page 83-86; 115pp; English.
XX This DNA sequence encodes the novel surface exposed protein Omp7
XX (see AAW88431) of Chlamydia pneumoniae, a human respiratory pathogen.
CC It is described below as a subsequence of a claimed nucleic acid fragment
CC (see AAX06819) encoding Omp7 (see AAW88420). The invention provides a
CC new species specific test for identifying mammals (including
CC humans) infected with C. pneumoniae. The test comprises detecting
CC antibodies specific for surface exposed proteins Omp4-Omp15 (see
CC AAW88417-28) or detecting nucleic acid fragments encoding them (see
CC AAX06816-27), especially by PCR. The proteins are also used in the
CC diagnosis of C. pneumoniae infection in mammals. The nucleic acids
CC and proteins can also be used in the immunization of mammals, the
CC nucleic acids being particularly useful as DNA vaccines for
CC effecting in vivo expression of antigens. The vaccines may also
CC prevent atherosclerosis and bronchial asthma, which are possibly
CC associated with C. pneumoniae.
SQ Sequence 1830 BP; 485 A; 357 C; 443 G; 545 T; 0 other;

Alignment Scores:
Pred. No.: 1,936-187 Length: 1830
Score: 2603.00 Matches: 532
Percent Similarity: 74.46% Conservative: 22
Best Local Similarity: 71.51% Mismatches: 50
Query Match: 60.61% Indels: 140
DB: 20 Gaps: 8

US-09-830-446-27 (1-841) x AAX06830 (1-1830)
QY 30 LeuSerAlaSerAsnSerPheAspGlyThrThrSerThrThrSerPheSerSerIys--- 48
DB 10 TTAGCGAGTCCGACAGTATATATGATGATCAACACACAGAAATTAATCTCTAAAGCG 69
QY 49 ThrSerSerAlaThrAspGlyThrAsnTyrValPheIysAspSerValValIleGluAsn 68
DB 70 GCACCTTTCGATGCTAGTGGCAGACCTATATTTTCGATGGGAGATCTCGATTAAGCCAA 129
QY 69 ValProIYrThrGlyGluThrGlnSerThrSerCysPheIysAsnAspAlaAlaIleGly 88
DB 130 GCAGGGAACAA---ACGAGCTTACCAACAAGTGTCTTTTCTTAC-----ACTGCAGGA 180
QY 89 AspLeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThr 108
DB 181 AATCTTACCTTCTTGGGACGAGATTTCTCTTCAATTTTGACAAATATATTTGCTACT 240
QY 109 AlaSerGlyAlaAlaIleGlySerGlnAlaAlaAsnIYsThrValThrLeuSerGlyPhe 128
DB 241 GTTGCAGGCTGTTGTTTTCGATACATACAGAGCTTTCGGATTAACAAATTTCTCAGGATTT 300
QY 129 SerAlaLeuSerPheLeuIYsSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
DB 301 TCACTCTTCGAGATCTTGCAGCTCTGAGACCAA----- 336
QY 149 AsnValIYsGlyAsnLeuSerLeuLeuAspAspIYsValIleuIleGlnAspAsnPhe 168
DB 336 ----- 336
QY 169 SerThrGlyAspGlyAlaIleAsnCysAlaGlySerLeuIYsIleAlaAsnAsnIYs 188
DB 336 ----- 336
QY 189 SerLeuSerPheIleGlyAsnSerSerSerThrArgGlyAlaIleHisThrIYsAsn 208
DB 336 ----- 336
QY 209 LeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAla 228
DB 336 ----- 336

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DR WPI: 2000-365569/31.
 P-PSDB: AAY94327.

XX Novel Chlamydia 98 kDa putative outer membrane protein antigen, used
 PT for vaccination and protection against Chlamydia infection
 XX

PS Claim 1, Fig 1, 93pp; English.

CC The present sequence is the 98kDa putative outer membrane protein gene
 CC from Chlamydia pneumoniae. The genomic sequence was amplified using two
 CC PCR primers. The 5' primer contains a NotI restriction site, a ribosome
 CC binding site, an initiation codon and a sequence close to the 5' end of
 CC the 98kDa putative outer membrane protein coding sequence. The 3' primer
 CC contains the sequence encoding the C-terminal sequence of the putative
 CC outer membrane protein and a BamHI restriction site. The stop codon was
 CC excluded and an additional nucleotide was inserted to obtain an in-frame
 CC C-terminal fusion with the Histidine tag. The PCR product was cloned
 CC into a eukaryotic expression vector (pCA-Myc-His) by restricting both
 CC the vector and the PCR product with NotI and BamHI and performing a
 CC ligation reaction. This expression vector was injected intramuscularly
 CC and intranasally into mice, which were subsequently inoculated with
 CC Chlamydia pneumoniae. The chlamydial lung titers of the immunised mice
 CC were lower than those of the controls. Thus the 98kDa putative outer
 CC membrane protein can be used as a vaccine to provide protection against
 CC Chlamydia infections, especially Chlamydia pneumoniae infections.
 CC The polypeptide may also be administered orally to treat Chlamydia
 CC infection. The present sequence may also be used in the
 CC construction of attenuated Chlamydia strains that can over-express the
 CC gene or express it in a non-toxic form.

Sequence 3000 BP; 871 A; 617 C; 634 G; 878 T; 0 other;

Alignment Scores:

Pred. No.:	7.75e-110	Length:	3000
Score:	1580.50	Matches:	375
Percent Similarity:	52.54%	Conservative:	121
Best Local Similarity:	39.72%	Mismatches:	306
Query Match:	36.80%	Indels:	142
	21	Gaps:	19

US-09-830-446-27 (1-841) x AAA27021 (1-3000)

QY 15 ThrLeuSerMetSerAenLeuEugLYAlaLathThrGluGluLeuSerAlaSerAen 34
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 134 AACTTTGCTATTTCCTTGTCTATGATGCTACCAAGACAGTTTGATTCACAGTGGC 193
 QY 35 SerPheAspGlyThrTherSerThrTherSerPheSerSerlyTherSerAlaThraap 54
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 194 AGTTTCGATGGG--AAATAAAATGTAATTTTCAGTTTCGTGAGAGTCAGGAAGATGCT 250
 QY 55 GlyThrAenTYValPheLYAspSerValValIleGluAenValProLYThrGlyGlu 74
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 251 GGAACTACTACTACTATTAAAGGAATGTCACCTCTGAAATAATCTCTGAAACAGGCACA 310
 QY 75 ThrGlnSerTherSerCySPheLYAspAenAlaAlaIleGlyAspLeuAenPheLeuGly 94
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 311 GCAATACAAAAAGCTGTTTAAACAC--ACTAAGGCGCATTTGACCTTCACAGGT 364
 QY 95 GlyGlyPheSerPheTherPheSerAenIleAspAlaThrThraLaseGlyAlaAlaIle 114
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 365 AACGGGAAGCTCTATATGTTCCAAACGGTGAATGACGGAGCTGTACAGGGGCTGTTT 424
 QY 115 GlySerGluAlaAlaAenLYThrValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 425 AACAGAGCGGTGTATATATCTACACAGTTTATGAGGGTTCCTTCGCTACTTTTATT 484
 QY 135 LySerPheAlaSerThraValThraGlyLeuGlyAlaIleAenValLYS--GlyAen 153
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 485 GCGTCTCTCGAGAGTTGATGATCTACCGGCAAGAGCCGTTAGCTGCTTACGGGTAGC 544
 QY 154 LeuSerLeuLeuAenAenAenLYValLeuIleGlyAenAenPheSerThraLYAspGly 173
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 545 TTGAGTTTGA CAATAATGTCAGTTGCTCTCAGCAAAAATTTTCAAGGATTAATGGC 604

QY 174 GlyAlaIleAenCys----- 178
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 605 GGTGCTATACCGCAAAAACTCTTTCATTAAACAGAGCTACATATGTGAGTCTGTTTCT 664
 QY 178 ----- 178
 DB 665 GAATAATACCTCTCAAGAAAGCGAGCATTCAGACTCCGATGCCCCATTACATTACT 724
 QY 178 ----- 178
 DB 725 GGAACCAAGGGAAGTCTTTTTCGACAAATCTTTCGANTTCGAGCTGCAATT 784
 QY 179 -----AlaGlySerLeuLYleAlaAenAenLYSerPheIle----- 193
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 785 TTTACAGAAAGCTCGGTACTATTCTTAATATGTAAGTTCTCTTATTGACAAATAG 844
 QY 193 ----- 193
 DB 845 GTCAAGAGGAGCTCTCAACAAAGGGATATGTCAGAGGTCATCTGCTTAT 904
 QY 194 -----Gly 194
 DB 905 AAAAAGTACTACAGTACTAAGTCACTCACTGAAATCAGATCTTCTTACGCAAC 964
 QY 195 AenSerSerThraGlyGlyAlaIleIleThraLYAenLeuThrLeuSerGly 214
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 965 AATCATGACACAAAGCGGAGAGCTATCTATGGAAGAAAGCTGAACTGCTCCGGA 1024
 QY 215 GlyLeuThraLeuPhe-----GlnGlyAenThraAlaProThraAlaGly 229
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1025 GGACTTACCTTATTCAGTAAGAAATAGTGTCAATGAGGTACAGTCCCT----- 1072
 QY 230 LYseGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1073 AAAGGTGAGCCATGCTATGAAATGAGGGAATGAGTTATCCGCGATATGCT 1132
 QY 250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr-----GlyThraValSerHisSer 267
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1133 GACATGCTCTTTTGGGAATACAGTCACTTCTACTCTCCCTGGAGC--AAATGAAGT 1189
 QY 268 AlaIleAspLeuGlyThrSerAlaLYleThraIleLeuArgAlaIleGlnGlyHisThr 287
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1190 AGTATCGACTTATGGAACAGATGCAAAAGATGACAGCTTTCGCTGCTGTAGAGCC 1249
 QY 288 IleTYrPheTYrAspProIleThraValThrGlySerThraValAlaAspAlaLeuAen 307
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1250 ATCTACTCTTATGATCCATTAATCTACAGATCATCAACAGTTACAGATGCTTAAAA 1309
 QY 308 IleAenSerProAspThrGlyAspAenLYSerGlyTYrThrIleValPheSerGly 327
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1310 GTTAATGAGACTCCGCGAGATTCGACTACATATACAGGAACATCATCTTACAGGA 1369
 QY 328 GlyLYLeuThrGluAlaGlyAlaLYAspGlyLYAspAenArgThrSerLYLeuLeuGln 347
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1370 GAAAAATTATCAGACAGAGCCGAGTTCTAAAAATCTTAATCTGAACTACTACAG 1429
 QY 348 AenValAlaPheLYAsnGlyThraValLYLeuLYAspValValLeuSerAlaAen 367
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1430 CCTGTAACTCTTTCAGAGGATCTATCTTAAACATGAGTCACTTGAAGTCTGAG 1489
 QY 368 GlyPheSerGluAspAlaAenSerLYLeuIleMetAspLeuGlyThrSerLeu--Val 386
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1490 GCATTCATCAACAGGACAGATTCGCTCGAAATGAGAGTGAAGTACTTGAAGCT 1549
 QY 387 AlaAenThraGlySerIleGlyLeuThraAenLeuGlyIleAenIleAspSerLeuArgAen 406
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1550 GGTGATCTAGACACATA-----AACAATTGGCATTAATCATCATGTTTATGACGGT 1603
 QY 407 GlyLYLYleLYLeuSerAlaAlaThraIleGlyLYAspIleArgIleAspArgPro 426
 DB ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : : ||| : : : : :
 1604 GCAGAAAGGCAAAAATATGAAACAAAGCTACGTCAAAAAATCTTATCTGGAACC 1663

OY	427	ValValLeuAlaLeuAlaSerAspGluSerPheTyrglnAsnGlyPheLeuAsnGluAspHis	446
DB	1664	ATCATCTTAATTGGACCCCAAGCGGCGTTTATGAAATCATAGTTTAAGAAATCTTCAG	1723
OY	447	SerTyraaPglYylLeuGlnLeuAspAlaGlyLysAspIleValIleSerAla--AspS	466
DB	1724	TCCATACGAC--ATCTTAGAGCTCAAAGCTTCTGGAACTGTAAACAAGCACCGCACTGACT	1788
OY	466	erArgSerIleAspAlaValGlnSerPro-TyrglyTyrglnGlyLysTrp---ThrIle	484
DB	1781	CCAGATCTCATATATGGGTGAGAAATTCATTTACGGCTATACAGGAACTTGGGGCCCAATT	1840
OY	485	AsnTrpSerThrAsp---AspLysLysAlaThrValSerTrpAlaLysGlnSerPheAsn	503
DB	1841	GTTTGGGGGACAGGGCGCTTCTACAGCTGAACTTCACCTGAGCTAAACCTGCGTATATT	1900
OY	504	ProThrAlaGlnGlnGlnAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp	523
DB	1901	CCTAATCCCGACCGATATGGCGCTCTTTAGCTCCTAATAGCTTATGGAAATGATATTATGAT	1966
OY	524	ValArgSerPheGlnAsnPheIleGlnLeuGlyTythrGlnGlyAlaProTyrglnLysArg	543
DB	1961	ATTAGCTCTCTCCATTAATCTTAATGAGACTGGAAACGAAGCTTCAGAGAGACCGTCT	2020
OY	544	PheTrpValAlaGlyIleSerAsnValLeuHisArgSerGlyArgGlnAsnGlnArgLys	563
DB	2021	TTTGTGTGTGGATTTATCTTAATCTTCCATTAAGATAGTACAAACAACAGCGCGGG	2088
OY	564	PheArgHisValSerGlyGlyValaValaGlyAlaSerThrArgMetProGlyLysAsp	583
DB	2081	TTTCCCATTTGAGTGGGGGATTATGATCATAGAGAAACCTACATCTTGCAGATTAAG	2140
OY	584	ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPheMetAsnThr	603
DB	2141	ATTCTTAGGCGCATTTTGTGCAGCTCTTGGAAAGATAGAGACTACTTTGTAGCTAAG	2200
OY	604	AsnPheAlaLysThrTyralaGlySerLeuArgLeuGlnHisAspAlaSerLeuTySer	623
DB	2201	AATCAAGGATCAGTCTACAGGAACCTCTATTACCGACACACGAACCTATATCTCT	2260
OY	624	ValValSerIleLeuLeuGlyGlnGlyLysArgGlnIleLeuLeuProTyValSer	643
DB	2261	CTTCCCTGCG-----AAACTACGCGCTTGTCTGCTGATCTTAATGTTCTT	2302
OY	644	LysThrLeuProCysSerPheTyrglyGlnLeuSerTyrglyHisLeuThrAspHisArgMet	663
DB	2303	ACAGAGATTCCTGCTCTCTTTCAGGAACCTTACTACACCCATACGGATTAACGATCTG	2362
OY	664	LysThrGlnSerLeuProProProProThrLeuSerThrAspHisLeuSerTrpGly	683
DB	2363	AAAAACAAGTAT-----ACAACATATCTTACTGTTAAAGAAAGCTGGGGG	2407
OY	684	GlyTyrValIleTrpAlaGlyGlnLeuGlyThrArg-----ValAlaValGlnAsnHisSer	701
DB	2408	AATGATAGTTCGCTTGAATTCGCTGGAAGAGCTCCGATTTGCTTGAATGAAGAAGTCT	2467
OY	702	GlyArgGlyPhePheGlnGlnTyThrProPheValLysValGlnAlaValTyralaArg	721
DB	2468	-----CATTTGAGCAGTACATGCCCTTCATGAAATATGGCATGTTGTCTATGACAT	2518
OY	722	GlnAspSerPheValGlnLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr	741
DB	2519	CAGGAAGCTTTTAAAGAACACAGGAACAGAAGCTCGTAATTTGGAAGTACGCGTCTCTG	2578
OY	742	AsnLeuAlaIleProLeuGlyIleLysLeuGlnLysArg-----PheAlaGlnGlnTyr	759
DB	2579	AATCTTGCTTACCTATCGGATCGGATTCGATTTGATTAAGATCAGACTCGCAAGATGCAAG	2638
OY	760	TyrrHisValAlaAlaMetTySerProAspValCysArgSerAsnProLysCysThrThr	779
DB	2639	TACATATCACTCTGTTATATCTGTGATCTCTTCTGTTAGTAAACCCGACTGTATACACA	2698
OY	780	ThrLeuLeuSerAsnGlnGlySerTrpLysThrLysGlySerAsnLeuAlaArgGlnAla	799

Db	2699	ACACTGGCAATTACCGGTGATTCTTGGAAAACTTCGGTACGAATTTGGCAAGCAAGCT	2758
Oy	800	GlyValGlnAlaSerGlyPheArgSerLeuGlyValAlaIleGluLeuPheGlyAsn	819
Db	2759	TTAGTCTTCGTGTGAGGAAACCATTTTGGCTTTACTCAAAATTTTGAAGCTTTAGCCAA	2818
Oy	820	PheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValIlePalaGlySerLeuIle	839
Db	2819	TTTTCTTTGGAATTCGTGGGTATCTCGCAATTAACATGTAGACTTAGAGCAAAATAC	2878
Oy	840	LysPhe 841	
Db	2879	CAATTC 2884	
RESULT 8			
ID	AAx06820	standard; DNA; 2787 BP.	
XX	AAx06820;		
AC	AAx06820;		
DT	26-APR-1999	(first entry)	
XX			
DB	Chlamydia pneumoniae surface exposed protein Omp8 DNA.		
XX			
XX	Omp8; outer membrane protein 8; surface exposed protein; antigen;		
KW	infection; diagnosis; vaccine; atherosclerosis; asthma; ss.		
XX			
OS	Chlamydia pneumoniae.		
XX			
FN	MO9856953-A2.		
XX			
PD	30-DEC-1998.		
XX			
PF	19-JUN-1998;	98MO-DK00266.	
XX			
PR	23-JUN-1997;	97DK-0000744.	
XX			
PA	(BIRK/) BIRKELUND S.		
PA	(CHR1/) CHRISTIANSEN G.		
PI	Birkelund S, Christiansen G, Knudsen K, Madsen A;		
PI	Myind P;		
XX			
PT	Species-specific test for identifying mammals infected with		
PT	Chlamydia pneumoniae - comprises detecting antibodies specific for		
PT	outer membrane proteins of C. pneumoniae or nucleic acids encoding		
PT	these proteins		
XX			
PS	Claim 6; Page 52-53; 115pp; English.		
XX			
CC	This DNA sequence codes for the novel 90.0 kDa surface exposed		
CC	protein Omp8 (see AAM88421) of the human respiratory pathogen		
CC	Chlamydia pneumoniae. By generating antibodies against C		
CC	pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)		
CC	was obtained which reacted with outer membrane proteins. The		
CC	antibody was used to identify the genes (see AAX06816-27) encoding		
CC	Omp4-Omp5 proteins (see AAM88417-28) in an expression library of		
CC	C. pneumoniae DNA. The genes are situated in 2 gene clusters:		
CC	Omp12,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in		
CC	the other, and encode polypeptides of about 89.6-100.3 kDa and		
CC	about 56.1 kDa. The invention provides a new species specific test		
CC	for identifying mammals (including humans) infected with Chlamydia		
CC	pneumoniae. The test comprises detecting antibodies specific for		
CC	Omp4-Omp5 or detecting nucleic acid fragments encoding these outer		
CC	membrane proteins, especially by PCR. The proteins are also used		
CC	in the diagnosis of C. pneumoniae infection in mammals. The		
CC	nucleic acids and proteins can also be used in the immunization of		
CC	mammals, the nucleic acids being particularly useful as DNA		
CC	vaccines for effecting in vivo expression of antigens. The		

CC vaccines may also prevent atherosclerosis and bronchial asthma,
 CC which are possibly associated with *C. pneumoniae*.

XX Sequence 2787 BP, 811 A, 583 C, 598 G, 795 T, 0 other;

Alignment Scores:

Pred. No.:	4,79e-109	Length:	2787
Score:	1569.50	Matches:	373
Percent Similarity:	52.33%	Conservative:	121
Best Local Similarity:	39.51%	Mismatches:	308
Query Match:	36.54%	Indels:	142
DB:	20	Gaps:	19

US-09-830-446-27 (1-841) x AAX06820 (1-2787)

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QY 15 ThrLeuSerMetSerAsnLeuGlyAlaIaThrThrGluGluLeuSerAlaSerAsn 34
DB      :::::
DB 34 ACAATTGCTAATTTCCCTTGTCTATGATGCTACCGAGACAGTTTGGATTCAAGTCG 93
QY 35 SerPheAspGlyThrThrSerThrThrSerPheSerSerThyThrSerSerAlaThrAsp 54
DB 94 AATTTCGATGCG---AATATAAATGTAATTTTTCAGTTTCGTGAGAGTCAGAAAGATGCT 150
QY 55 GlyThrAsnTyValPheIysAspSerValIleGluAsnValProIySerThyGlyGlu 74
DB 151 GGAATCTACTACTATTAAGGAAATGTCATCTGAATAATATTCCTGGACAGGCACA 210
QY 75 ThrGlnSerThrSerGlyPheIysAsnAspAlaAlaGlyIAspLeuAsnPheLeuGly 94
DB 211 GCATCTCAAAAGAGCTTTTAAACAC-----ACTAAGGCGCATTTGACTTTCACAGCT 264
QY 95 GlyIyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIle 114
DB 265 AACGGAACTCTCTATTGTTCCAAACGGAGATGCGAGACTGTACAGGCGCTGCTGT 324
QY 115 GlySerGluAlaAlaAsnTyValThrLeuSerGlyPheSerAlaLeuSerPheLeu 134
DB 325 AACAGCAGCGGTGGTAATAATCTACACAGTTTATAGGGTTTCTCGCTATCTTTATT 384
QY 135 LysSerProAlaSerThyValThraAsnGlyLeuGlyAlaIleAsnValIys---GlyAsn 153
DB 385 GCGTCCCTCGAAGTTCGATTAACCGGCAAGGCGCGTGAAGCTCTCAAGCGGTAC 444
QY 154 LeuSerLeuLeuAspAsnAspLysValLeuIleGluAspAsnPheSerThyGlyAspGly 173
DB 445 TTGAAGTTGACAAAAATGTCAGTTTCTCTTCAGCAAAACTTTTCAAGGATATGCG 504
QY 174 GlyAlaIleAsnCys----- 178
DB 505 GGTGCTATCACCGCAAAAATCTTTTCAATTACAGGATCAATGTCAGCTGTGTTCT 564
QY 178 ----- 178
DB 565 GAAATACCTCTCAAGAAAGCGAGCGACATTCAAGTTCGATCCCTTACATTACT 624
QY 178 ----- 178
DB 625 GGAACCAAGGGAGAGTCTTTTCTGACAAATCTTTCGAGATTCTGAGCTGCATT 684
QY 179 -----AlaGlySerLeuIysIleAlaAsnAsnIysSerLeuSerPheIle----- 193
DB 685 TTTACAGAAAGCCCGGTGACTATTTCTAATATGCTAAAGTTTCTTTATTCACATAAG 744
QY 193 ----- 193
DB 745 GTCAACAGAGCAGCTCTCAACACGCGGATATGTCAGAGTGTCTATCTGTCTTAT 804
QY 194 -----Gly 194
DB 805 AAAACCTAGTACATCTAAGGTACACCTCTCACTGAAATCAGATGTTACTTTCAGCAAC 864
QY 195 AasnSerSerThrArgGlyGlyAlaIleKilSerThyAsnLeuThrLeuSerGly 214
DB      :::::

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DB 865 AATACATGACAAACAGCGGAGAGCTATCTATGTGAAGAAAGCTGAACCTGCTCCGA 924
QY 215 GlyIuThrIlePhe-----GlnGlyAsnThrAlaProThrAlaIleGly 229
DB 925 GGAATTAACCTTAATAGTAAGAAATAGTGTCAATGAGGTACAGCTCTC----- 972
QY 230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
DB 973 AAAGGTGAGACCATAGCTATTCGAAGATAGTGGAAATTGAGTTTATCCGCGATAGTGT 1032
QY 250 AspIleIlePheGluGlyAsnThrIleGlyAlaThr-----GlyThrValSerHisSer 267
DB 1033 GACATGTCTTTTATGGAATACAGTCACTTCTACTACTCCCTGGAGCG---AATGAAGT 1089
QY 268 AlaIleAspLeuGlyThrSerAlaIleThrAlaLeuArgAlaIleGlnGlyHisThr 287
DB 1090 AGTATGACCTTAAGAACAGATGCAAAAGATGACAGCTTTCGCTGCTGTGAGAGCC 1149
QY 288 IleTyPheTyAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
DB 1150 ATCTACTCTATGATCCCATATCTACAGATCTTCCACACAGCTTACAGATGCTTAAAA 1209
QY 308 IleAsnSerProAspThrGlyAspAsnLysGlyTyThrGlyThrIleValPheSerGly 327
DB 1210 GTTAATGAGACTCCGCGAGATTCTGACTACATATACAGGAGATCATCTTTCACAGGA 1269
QY 328 GlyIyIleuThrGluAlaGluAlaIysAspGlyIyAspAsnArgThrSerIyIleuGln 347
DB 1270 GAAAAGTTATCAGACACAGAGCGCGAGATTTTAAAAATCTTACTTCGAGCTACTACAG 1329
QY 348 AsnValAlaPheIyAsnGlyThrValValIleuIyGlyAspValIleuSerAlaAsn 367
DB 1330 CCTGTACTCTTTCAGAGAGTACTATCTTAAACATGAGATGACTCTGAGACTCAG 1389
QY 368 GlyPheSerGlnAspAlaAsnSerIyLeuIleuIleuIleuIleuIleuIleuIleuIleu 1449
DB 1390 GCATTCACCTCAACAGGAGATTTCTGCGAAATGAGCGTGAAGAACTTCAAGACT 1499
QY 387 AlaAsnThrGlnSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsn 406
DB 1450 GGTATTAATCAGACCATAT-----AACATTTGTCATTAATCATGATCTTATTAACGCT 1503
QY 407 GlyIyIyIleIyLeuSerAlaIleAlaThrAlaGlnIyAspIleArgIleAspArgPro 426
DB 1504 GCAAGAAAGCGCAAAATATGAACCAAGCTACGTCAAAATATCTGACTTATCTGGAAC 1563
QY 427 ValValIleuAlaIleSerAspLysSerPheTyGlnAsnGlyPheLeuAsnGluAspHis 446
DB 1564 ATCACTTATTGACCCGACCGGCGAGTTTATGAATAATCATAGTTTAAAGAAATCCTCAG 1623
QY 447 SerTyTrpAspGlyIleLeuGluLeuAspAlaGlyIyAspIleValIleSerAla--AspS 466
DB 1624 TCTTACGAC--ATCTTGAAGCTCAAAAGCTTCTGAACTGTAAACAGCACCGCATGACT 1680
QY 466 eArgSerIleAspAlaValGlnSerPro--TyrgIyTyrgIyGlnIyIySerPro---ThrIle 484
DB 1681 CCAAGTCTCATTAATGGGTGAAGAAATTCATTAACGCTTACAGGAACTTGGGCGCAATT 1740
QY 485 AsnTPSerThrAsp---AspIyIyAlaIleThrValSerTPAlaIyGlnSerPheAsn 503
DB 1741 GTTGGGGGACAGGGGCTTCTACAGCTCAACCTTCACTGAGCTTAAACCTGGCTATATT 1800
QY 504 ProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp 523
DB 1801 CCTAATCCGAGCGTATGCGCTCTTATGCTTAACTTATGGAATGATCATTTATAGT 1860
QY 524 ValArgSerPheGlnAsnPheIleGluLeuGlyThrGlnGlyAlaProTyrgIyIyAsnArg 543
DB 1861 ATTACTCTCTCCATTAATCTTATGAGAGCTGCAACGAAAGGTTTCAGAGAGACCTGTCT 1920
QY 544 PheTyValAlaGlyIleSerAsnValIleuHisArgSerGlyIyAsnGluAsnGlnArgIyS 563
DB 1921 TTTGTGTGTGCTGATATCTTATCTTCTTCAATAGATAGTAAACAAACAGCAGCGCGG 1980

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QY 564 PheArgHisValSerGlyGlyAlaValAlaGlyAlaSerThrArgMetProGlyGlyAsp 563
DB 1981 TTTCGGCATTTGAGTGGCGGTATGTCATAGAGAAACCTACCTACTGTCAGATTAAG 2040
QY 584 ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspIleAspIlePheMetAsnThr 603
DB 2041 ATTCTTAGTGTCTGCAATTTTGTCTCTTGTGGAAGATGAGCTACTCTTTAGTGAAG 2100
QY 604 AsnPheAlaIleThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSer 623
DB 2101 AATCAAGGTACAGTCTACGAGAGAACTCTATTATACGACAAACCAACCTATATCTCT 2160
QY 624 ValValSerIleLeuLeuGlyGlyGlyGlyLeuArgGlyIleLeuLeuProTyrValSer 643
DB 2161 CTTCCTTGC-----AACTAGCGGCTGTGCTGTCTATGTTCCCT 2202
QY 644 LysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMet 663
DB 2203 ACAGAGATTCCTGTTCTCTTTTCAAGAAACCTTAGCTACACCATACGAGTAACGATCTG 2262
QY 664 LysThrGlySerLeuProProProProProThrLeuSerThrAspHisThrSerTyrGly 683
DB 2263 AAAACCAAGTAT-----ACAACATATCTCTGTTTAAAGAACCTGGGG 2307
QY 684 GlyTyrValTyrAlaGlyGlyLeuGlyThrArg-----ValAlaValGluAsnThrSer 701
DB 2308 AATGATGATTTCCCTTAGAATTCGGTGAAGAGCTCCGATTTGCTTAGATGAAGTCT 2367
QY 702 GlyArgGlyPhePheGlnGlyTyrThrProPheValIleValAlaValTyrAlaArg 721
DB 2368 -----CTATTGAGCAGTACATGCCCTTCATGAAATTGACAGTTGTCTATGACAT 2418
QY 722 GlnAspSerPheValGlyLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyr 741
DB 2419 CAGGAAGGTTTAAAGAACGAGAAACGAGAGCTGTAATTGGAAGTACCCGCTTTGTG 2478
QY 742 AsnLeuAlaIleProLeuGlyIleLeuValLeuGlyLeuArg-----PheAlaGlnGlnTyr 759
DB 2479 AATCTTGCCCTTACTCTACCGGATCCGATTCGATTAAGAAACACAGCTCCCAAGTCAAG 2538
QY 760 TyrHisValAlaIleMetTyrSerProAspValCysArgSerAsnProIleCysThrThr 779
DB 2539 TACAACTAACTCTGTTGTTATCTGATGAGACTGTTGTTGATGTAACCCGACTGACGACA 2598
QY 780 ThrLeuLeuSerAsnGlnGlySerTyrPheThrIleGlySerAsnLeuAlaArgGlnAla 799
DB 2599 ACACTCGAAATTGACCGGTGATCTTGGAACCTTCGGTACGAATTTGGCAAGACAGCT 2658
QY 800 GlyIleValGlnAlaSerGlyPheArgSerLeuGlyValAlaIleAlaGlyLeuPheGlyAsn 819
DB 2659 TTAGTCTCTCGTCAAGGAACCATTTTGCTTTAACTCAAAATTTTGAAGCTTTAGCCAA 2718
QY 820 PheGlyPheGlyIleTyrArgIleSerSerArgSerTyrAsnValAlaSerIleGlySerIle 839
DB 2719 TTTCTTTTGAATTGCGTGGTCACTCGCAATTACAACTTAGACTTAGAGAGCAAAATAC 2778
QY 840 LysPhe 841
DB 2779 CAATTC 2784

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RESULT 9

ABQ84758 standard; DNA; 2520 BP.

ABQ84758;

25-FEB-2003 (first entry)

Chlamydia psittaci antigen CP#4 encoding DNA SEQ ID NO:22.

Chlamydia psittaci; vaccination; vaccine; antigen; immune response; immunisation; antibacterial; infection; gene; ds.

```

XX OS Chlamydia psittaci.
XX FH Key Location/Qualifiers
XX FT CDS 1..2520
XX FT /tag= a
XX FT /product= "antigen CP#4"
XX PN MO200253588-A2.
XX PD 11-JUL-2002.
XX PF 17-DEC-2001; 2001MO-US48715.
XX PR 15-DEC-2000; 2000US-0738269.
XX PA (TEXA ) UNIV TEXAS SYSTEM.
XX PI Johnston SA, Stenke-Hale K, Sykes KF, Kaltenboeck B;
XX PI WPI: 2002-537942/57.
XX DR P-PSDB; ABP56002.
XX PT Vaccine for immunization of animal, preferably bovine, against
XX PT Chlamydia psittaci, comprises at least one polynucleotide having a C.
XX PT psittaci sequence, or at least one C. psittaci antigen
XX PS Claim 14, Page 126; 164pp; English.
XX CC The present invention describes a vaccine (I) for the immunisation of an
XX CC animal against Chlamydia psittaci comprising at least one polynucleotide
XX CC (Ia) having a C. psittaci sequence, or at least one C. psittaci antigen
XX CC (Ib), and a carrier. (Ia) and (Ib) have antibacterial activity. (I) is
XX CC useful for the immunisation of a bovine. The present sequence encodes a
XX CC C. psittaci antigen from the present invention.
XX SQ Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;
XX
Alignment Scores:
Pred. No.: 1,29e-103 Length: 2520
Score: 1497.00 Matches: 357
Percent Similarity: 56.21% Conservative: 132
Best Local Similarity: 41.03% Mismatches: 321
Query Match: 34.85% Indels: 60
DB: 24 Gaps: 25
US-09-830-446-27 (1-841) x ABQ84758 (1-2520)
QY 1 MetIleIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
DB 1 ATGAACATCCAGTCTACTGTTCTTAATATCC-----TCAGCCTATTGCTCGAAT 54
QY 21 LeuLeuGlyAlaAlaThrThrGlnGlu-----IleSerAlaSerAsnSerPheAspGly 38
DB 55 TCTTTGAGCTCGCTCAACAGCGCTCAACAGCCTTAATCCCTCCGATGATTAATGGA 114
QY 39 ThrThrSerThrThrSerPheSerSerIleTyrSerSerAlaThrAspGlyThrAsnTyr 58
DB 115 AATGTACCTCTGAGAGAGTTCCAGGTAAAGAAATTCATCA-----GGAACACGTAAT 168
QY 59 ValPheLysAspSerValAlaIleGluAsnValProLysThrGlyGlyIleThrGlnSerThr 78
DB 169 ACTTGGAAGGCAATGTGTATCTCTTGCAGGAGAAAGATTCAAGTCTTAAGAAA--- 225
QY 79 SerCysPheLysAsnAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyIlePheSer 98
DB 226 AGTTGTTTC-----TCAGCTACTGATTAACCTTAACCTTCTTAGAGAAACGGGTATACT 276
QY 99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlyAla 118
DB 277 CTTCCTTTGATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 336
QY 119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138

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Db 337 CAAGGAAAACCTTAGCATCTCAGAGATTCTTATTTTCATGCTTATGCTTCA 396
Qy 139 SerThrValThrAsnGlyLeuGlyValAlaIleAsnVallyrGlyAsnLeuSerLeuLeuAsp 158
Db 397 GGC-----ACACGTGGTTACGAGACTATACAGACTAAAGGCACACAACTTAAAGAT 450
Qy 159 AsnAspLyValLeuIleGlnAspAsnPheserThrGlyAspGlyGlyAlaIleAsnCyS 178
Db 451 AACTCTATCTTGTCTTCCATTAATAAGCTCTCAACAGCAAGAGGGGGCTATTCAGAGT 510
Qy 179 AlaGlySer-----LeuLySIIleAlaAsnAsnLySerLeuSerPheIleGly 194
Db 511 AAAGGAGACAGATGATGCTGAATTAAATAAGAAATAATACAGAACTGGTTTTCACAA 570
Qy 195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLyAsnLeuThrLeuSerSerGly 214
Db 571 AACTCTCCACTTCAAAAGCGGGCTATTATATGCTGATTAACCTCACATATGCTCAGGT 630
Qy 215 GlyIuThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly---LyGlyGlyAla 233
Db 631 GGGCTTACATTAATTTCTTCAACACTCTGTATCCAAAGGTTCAATCCCTTAAAGCGGAGCT 690
Qy 234 IleAlaIleAlaAsp---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
Db 691 ATTAGCATTAAGATTCAGATGCTGATGATGATGCTTACCGGCTGATCTCGAGATATTAC 750
Qy 253 PheGlnGlyAsn-----ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
Db 751 TTCGATGGGAACAAATCATCAAACTAGTGTGAGAACTTCTACAGTAAAGAAATTC 810
Qy 269 IleAspLeuGlyThrSerAlaLySIIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
Db 811 ATAGATCTGGGACAC---GGAAATTTACAAAGCTACGCTTAAAGCGGCTTCGAAAT 867
Qy 289 TyrPheTyAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
Db 868 TTCTCTATGACCTTATTAATCTGGGAGAGATCT-----GATGAATTAACATTT 915
Qy 309 AsnSerProAspThrGlyAspAsnLySIIleGlyThrGlyThrIleValPheSerGlyGlu 328
Db 916 AATAAATAAGAAACGTGTGAT-----TATACAGAAAGATGCTCTTCCAGGTAA 966
Qy 329 LysLeuThrGluAlaGluAlaLyAspGlyLyAspAspArgThrSerLyLeuLeuGlnAsn 348
Db 967 AATTTATCGATGAAGAAAGAAAGCAGAGCGAAACCTAGCTTCTTACCTTACCAACCA 1026
Qy 349 ValAlaPheLyAsnGlyThrValIleLeuLySIIleAspValIleLeuSerAlaAsnGly 368
Db 1027 ATCAATTAATACGAGATCTCTGTATCTTAAAGATGGTATCTGTAAACGCAAAACA 1086
Qy 369 PheSerGlnAspAlaAsnSerLySIIleLeuMetAspLeuGlyThrSerLeu----- 385
Db 1087 GTAAGCGAGAAAGCGGATCTACCGTGTATGATGATGATGATGATGATGATGATGAT 1146
Qy 386 ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
Db 1147 TCTTAGGCTGAGAAACATCACTCACTAATATCTAGATATTAACATGCGCTGTGGGG 1206
Qy 406 AsnGly-----LySIIleLySIIleLySIIleSerAlaAlaThrAlaGlnLyAspIleArg 422
Db 1207 GGGGGGGGGGGGACCTCTCTGCTTAACTCGCAACAAATACAGCAAGCTACATTA 1266
Qy 423 IleAspArgProValIleLeuAlaIleSerAspGlySerPheTyGlnAsnGlyPheLeu 442
Db 1267 ATTAAC---GCTGTCAATCTAGCTGATGCTGATGCTGATGCTGATGCTGATGCT 1323
Qy 443 AsnGluAspHisSerTyAspGlyIleLeuGluLeuAspAlaGlyLyAspIleValIle 462
Db 1324 GGTAGCTTAAACCTTTCACAGCAATAGTAGCTACAACTAACGCTAGTACAGTCA 1383
Qy 463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyGlyTyGlnGlyLyAspTyr 482

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Db 1384 CTTACAGATATATCTAACAAATTATATGCTCTCTACTCATTAACGTTACCAAGAAATGG 1443
Qy 483 ThrIleAsnTyrSerThrAsp-----AspLySIIleAlaThrValSerThrAlaLySIIle 500
Db 1444 ACAGTATCTTGGGACACCGAAACAGCTACAAACAAAGCCACTTACACTTGGGAAACAACT 1503
Qy 501 SerPheAsnProThrAlaGlnGluAlaProLeuValProAsnLeuLeuTyrGlySer 520
Db 1504 GGTACTCCCTTACCCAGAAACGTCAGAGACCTTATAGCCGAATACTCTTGGGGTGCA 1563
Qy 521 PheIleAspValIleSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540
Db 1564 TTCTCTACCTCAGAGGATATACAAACTTAATGATATAGATATAGCGTCAATGGGCTGACTAC 1623
Qy 541 GluLyAspPheThrValAlaGlyIleSerAsnValIleHisArgSerGlyArgGluAsn 560
Db 1624 CATAGAGCTTTTGGATATCGGCTAGCTAGCTTCTTACCAAAAGTGGCTCGATACT 1683
Qy 561 GlnArgLyAspPheArgHisValSerGlyValAlaValAlaGlyAlaSerThrArgMetPro 580
Db 1684 AAACGCAAGTTCCGTCACAAATAGCGCGGATAGCGCTTAAAGCGTACGCAAAACCTCT 1743
Qy 581 GlyIleAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLyAspTyrPhe 600
Db 1744 TCTGATGATATTTCAATGCGGCTTCTGCGCACTCTCGGAAAGGACAAAGACTATTTA 1803
Qy 601 MetAsnThrAsnPheAlaLySIIleThrTyAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db 1804 GTGTGCAAAACAAAGCCACATTTAGCGAGTCTCTATTAATACAGCA---ATCTCC 1860
Qy 621 LeuTySerValIleSerIleLeuLeuGlyGluGlyLeuArgGluIleLeuLeuPro 640
Db 1861 TATTGGAC-----GCTTGGCAAGATCTGCTCAAAAC 1893
Qy 641 TyrValSerLyThrLeuProCysSerPheTyGlyGlnLeuSerTyGlyHisThrAsp 660
Db 1894 ACTATCGGTGAGAAAGCTCGGTAGCTTAAACGACAGATTAATATGTCATGCTTCA 1953
Qy 661 HisArgMetLySIIleGlu-----SerLeuProProProProThrLeuSerThr 677
Db 1954 AACGACATGAAGAAACCAATGACATGATACCTTACCTCTGTAACCACTATGCGAA 2013
Qy 678 AspHisThrSerTyGlyGlyTyThrValIleAlaGlyGluLeuGlyThrArgValAlaVal 697
Db 2014 ATCAAGGCTATTTGGGTGAACGATTTGTCGAGTCAAGCTTGGCAACGTGCTATC 2073
Qy 698 GluAsnThrSerGlyArgGlyPhePheGlnGlyTyThrProPheValLySIIleAla 717
Db 2074 CAACAGATCTTCTCTC---CTATTGATATGATCACTCACTTCTGCAAGCTTCAACTT 2130
Qy 718 ValTyAlaArgGlnAspSerPheValGluLeuGlyAla---IleSerArgAspPheSer 736
Db 2131 GTGATACGACCAAGATGACTTAAGGAAACAAATAGCGATCAGGAGGATACTTGAA 2190
Qy 737 AspSerHisLeuTyAsnLeuAlaIleProLeuGlyIleLySIIleGluLyAspPheAla 756
Db 2191 AGCAGCAATCTCACCAACCTTCTCTGCTATCGGCATCAAGTTGAG---AGATTTCCT 2247
Qy 757 GluGln-----TyTyHisValAlaIleMetTySerProAspValCysArgSer 773
Db 2248 AACAAAGATACAGCTTCTTATCATGTCACTGCTCTTATTTCTCGATATGTAAAGAGT 2307
Qy 774 AsnProLySIIleThrThrThrLeuLeuSerAsnGlnGlySer-----TyrLySIIleThrLyS 791
Db 2308 AACCTGACTGATCTTCTCTGTGTAGTAAAGCCCACTGCTGCTGTGGGTAAAGAA 2367
Qy 792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
Db 2368 GCCAAACACTTGGCGCAAGGCGCTTCACTACAGAGAGAAACTACTTCTTTAACT 2427
Qy 812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyThrArgGlySerSerArgSerTy 831
Db 2428 CACAACATAGAAATCTTACGACGATTCGTTTCAAGCTCAGGGGATCTTCAAGAACCTAT 2487

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QY 832 AsnValaspAlaGlySerIySileIySeph 841
 DB 2488 AACGTAGATCTCGATCGAAGATCCAGTTC 2517

RESULT 10

ID ABQ78016 standard; DNA; 2520 BP.

AC ABQ78016;

DT 03-OCT-2002 (first entry)

DE Chlamydia polynucleotide SEQ ID NO 22.

KM Chlamydia; antibacterial; vaccine; immune response; infection; gene; ds.

OS Chlamydia psittaci.

PN WO200247718-A2.

PD 20-JUN-2002.

PF 17-DEC-2001; 2001MO-US48773.

PR 15-DEC-2000; 2000US-255839P.

PA (TEXA) UNIT TEXAS SYSTEM.

PI Johnston SA;

XX WPI; 2002-583472/62.

DR P-PSDB; ABB98211.

PT Vaccine useful for immunizing an animal, comprising at least one polynucleotide having a Chlamydia sequence or at least one Chlamydia antigen

PS Claim 6; Page 133-134; 183pp; English.

XX The invention relates to a vaccine (I) comprising at least one polynucleotide (ABQ78008-ABQ78039) having a Chlamydia sequence or at least one Chlamydia antigen (ABB98203-ABB98234) and a pharmaceutically acceptable carrier. The antigens are useful for immunizing an animal, by providing at least one Chlamydia antigen or its antigenic fragment to the animal, in an amount effective to induce an immune response in the animal e.g. mammals including bovine or human. The method is effective to induce an immune response against C. psittaci, C. pneumoniae or non-Chlamydia infection. The method further involves administering to the animal an antigen or an antigenic fragment from Chlamydia species other than C. psittaci or C. pneumoniae or an antigenic fragment from a non-Chlamydia species.

XX Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;

Alignment Scores:

Pred. No.:	1,29e-103	Length:	2520
Score:	1497.00	Matches:	357
Percent Similarity:	56.21%	Conservative:	132
Best Local Similarity:	41.03%	Mismatches:	321
Query Match:	34.85%	Indels:	60
	24	Gaps:	25

US-09-830-446-27 (1-841) x ABQ78016 (1-2520)

QY 1 MetIyEiIAProLeuNrgPheLeuLeuIleSerLeuValProThrIleuSerMetSerAan 20
 DB 1 ATGAACATCTCGATCGTCTTAATATCC-----TCGAGCCTAATTGCGCTGAAT 54
 QY 21 LeuLeuGlyAlaIalalThrIrgIuGlu-----LeuSerAlaSeruSerPheLeuApGly 38
 DB 55 TCTTTAGCTTGGCTTAACGACGCTCAAAACAGCCTTAATCTCCCTCGATAGCTATATAGGA 114

QY 39 ThrThrSerThrThrSerPheSerSerIyThrThrSerSerAlaThrAspGlyThrAenIy 58
 DB 115 AATGTACTCTGAGAGATTCCAGTAAAGAAACTATCA-----GGAAACAGTAT 168
 QY 59 ValPheIyAspSerValIalIleGluAenValProIyThrGlyIuThrGlnSerThr 78
 DB 169 ACTTGGAAGCAATGTGTATCTCTTCCTTGCAGGAAAGATTACAGTCTAAAGAAA--- 225
 QY 79 SerCyPheIyAsnAspAlaIalIalIyAspLeuAsnPheLeuIyGlyIyPheSer 98
 DB 226 AGTGTGTTCT-----TCAGCTACTGATTAACCTTACCTTCTGGAAGCGGTATCT 276
 QY 99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIalIleGlySerGluAla 118
 DB 277 CTGTGCTTGATATATATTAATCTACTACAGTAAACCCGAGGACATTAATGTTAAGGT 336
 QY 119 AlaAsnIyThrValThrIleuSerGlyPheSerAlaIleuSerPheLeuIySerProAla 138
 DB 337 CAAGGAAAACCTTAGGCATCTCAGGATTTCTTAATTTTCATGTGCTTAATGTCCTCCA 396
 QY 139 SerThrValThrAsnGlyLeuGlyAlaIleAenValIyAsnIleuSerIleuAsp 158
 DB 397 GGC-----ACAACGTGTACGAGCTATACAGACTAAAGCAACACATTTAAAGAT 450
 QY 159 AsnAspIyValIleuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAenCyS 178
 DB 451 AACTGATGCTGTCTTCATAAACCTGCTCAACGACGAAAGTGCGGCTATCCAGTGT 510
 QY 179 AlaGlySer-----LeuIySileAlaAsnAsnIySerIleuSerPheIleGly 194
 DB 511 AAAGGAAGCAGTACGTGAATTAATAAATAAGAAATATATCAGAAATGTGTTTCTCAGA 570
 QY 195 AsnSerSerSerThrArgGlyAlaIleIleIsthIyAsnIleuThrIleuSerSerGly 214
 DB 571 AACTCTCCACTTCACAAAGCGCGGTATTAATGCTGATTAACCTACCACTGCTCAGGT 630
 QY 215 GlyIuThrIleuPheGlnIyAsnThrAlaProThrAlaIalGly---LysGlyGlyAla 233
 DB 631 GGGCCACATTAATTTTCTAACAACCTGTATCCAACGGTCAATCCCTTAAGCGGAGGT 690
 QY 234 IleAlaIleAlaAsp---SerGlyThrIleuSerIleSerGlyAspSerGlyAspIleIle 252
 DB 691 ATTAGCATTAAGATTCAAGTGTGATGTATGATCTTAACCGCTGATCTCGAGATATTACC 750
 QY 253 PheGlnIyAsn-----ThrIleGlyAlaThrGlyThrValSerIleSerAla 268
 DB 751 TTCGATGGGAACAAATCATCAAACTAGTGTGGAAGTTCTTACGTAACAAGAAATTC 810
 QY 269 IleAspLeuGlyThrSerAlaIySileThrAlaIleuArgAlaIalGlnIyIsthIle 288
 DB 811 ATAGATCTCGGACA---GGGAATTTTACAAAGCTACGTGCTTAAGACGGCTTCGGAAT 867
 QY 289 TyrPheTyrAspProIleThrValThrIyGlySerThrSerValAlaAspAlaIleuAsnIle 308
 DB 868 TCTTCTATGACCTATTAATCTGCGGAGGATCT-----GATNAACATAAACAAT 915
 QY 309 AsnSerProAspThrGlyAspAsnIySglIyThrIrgIyThrIleValPheSerGlyIu 328
 DB 916 AATTAATAAAAGAACCTGTAT-----TATACGGAAGAGTCTCTTCTCAGGTGA 966
 QY 329 IySleuThrGluAlaGluAlaIyAspGlyIyAsnArgThrSerIySleuLeuGlnAen 348
 DB 967 AATTTATCCGATGAAGAAAGAACGACGGAAGAAACCTGATCTTAATCAACCAACCC 1026
 QY 349 ValAlaPheIyAsnGlyThrValIalIleuIySglIyAspValIalIleuSerAlaAsnGly 368
 DB 1027 ATCACATTATACGACGATCTCTTGAATTAAGATGAGTATCTGTAACCCGAAACAA 1086
 QY 369 PheSerGlnAspAlaAsnSerIyLeuIleMetAspLeuGlyThrSerIy----- 385
 DB 1087 GTTACCGACGAAGCGGATCTACCGTTCATGATGATCTTGAAGCAACATTAACAGCGCT 1146
 QY 386 ValAlaAsnThrGluSerIleGluIleuThrAsnLeuGluIleAsnIleAspSerIleuArg 405

[illegible]

Db 2191 AGCAGCATCTCCACCAACCTTCTCTCGCTATCGGCATCAAGTTTGAG--AGATTGGCT 2244
 Qy 757 GIuGIn-----TYrYrHisValaAlaMetYrSerProAspValCyaArgSer 773
 Db 2248 AACAAAGCATACAGCTCTTATCATGTCAGTCTGCTCTTATTTCTCTGATATGTAAGAAGT 2307
 Qy 774 AsnProIysCyGThrTrpThrThleuLeuSerAsnIndIngIser-----TrpIleThrIys 791
 Db 2308 AACCTTGACGTACTACTCTCTCTTGTAGTAAGCCCGACCTTGCTGTGGGTACGAA 2367
 Qy 792 GlysSerLeuLeuAlaArgGlnAlaGlyIleValaGlnIaSerGlyPheArgSerLeuGly 811
 Db 2368 GCCAACAACTCTGGCGCAAGGCCCTTCATGCTACAGCAGAAACACTTGTCTTTAAGT 2422
 Qy 812 ALAAlaAlaGluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerYr 831
 Db 2428 CACAACATATAGAAATCTTCAGCCAGTTCGGTTTCAGCTCAGGGGATCTTCACGAACCTAT 2487
 Qy 832 AsnValAspAlaGlySerIysIleLeuPhe 841
 Db 2488 AACGTAGATCTCGATCGAAGATCAAGTTTC 2517
 RESULT 11
 ID ABE99183 standard; DNA, 2520 BP.
 XX ABE99183;
 AC
 XX ABE99183;
 DT 20-MAY-2003 (first entry)
 DE C. psittaci genomic DNA sequence CP4 #4 #2.
 XX
 XX DNA vaccine; chlamydia infection; blindness; mastitis; infertility;
 KW abortion; sexually transmitted disease; atherosclerotic plaque; ds;
 KW community-acquired pneumonia; coronary heart disease.
 KW Chlamydia psittaci.
 OS
 XX Chlamydia psittaci.
 XX
 XX US200218372-A1.
 XX
 PD 05-DEC-2002.
 XX
 PF 17-DEC-2001; 2001US-0023437.
 XX
 PR 16-AUG-2000; 2000US-225839P.
 XX
 PA (JOHN/) JOHNSTON S. A.
 PA (STEM/) STEMKE-HALE K.
 PA (SYKE/) SYKES K. F.
 PA (KALT/) KALTENBOECK B.
 XX
 PI Johnston SA, Stemke-Hale K, Sykes KF, Kaltenboeck B;
 DR WPI; 2003-328634/31.
 XX P-PSDB; ABE06267.
 XX
 PT New vaccine comprising a polynucleotide with a Chlamydia sequence or a
 PT Chlamydia antigen, for inducing an immune response against Chlamydia
 PT psittaci, Chlamydia pneumoniae, other Chlamydia species, or a
 PT non-chlamydia infection -
 XX
 PS Claim 6; Page 46-47; 100pp; English.
 XX
 CC The invention relates to a vaccine comprising a pharmaceutical carrier
 CC and at least one polynucleotide having a Chlamydia sequence or at least
 CC one Chlamydia antigen. The polynucleotide sequences are obtained
 CC from cloned expression library of fragmented genomic DNA (expressed in
 CC the vector pCMV-Ub1(+P3). Also included are immunising an animal
 CC comprising providing to the animal at least one Chlamydia antigen or its
 CC antigenic fragment (expressed from the cloned polynucleotides) to induce
 CC an immune response (the proteins are chosen by transforming a vertebrate
 CC animal with constituents of the library and choosing those which elicit
 CC the best immune response, and then expressing those clones in cell

CC culture and purifying the protein), preparing antibodies against a
 CC Chlamydia antigen (comprising identifying a Chlamydia antigen that
 CC confers immune resistance against chlamydia bacterial infection when
 CC challenged with the Chlamydia species in which the antigen was prepared,
 CC generating an immune response in a vertebrate animal with the identified
 CC antigen, and obtaining antibodies produced in the animal, the antibodies
 CC are used to assay for the presence of chlamydia infection in a vertebrate
 CC animal) and testing for antigens for a first disease state/infectious
 CC agent (comprising determining an antigenic polypeptide or a nucleic acid
 CC encoding an antigenic polypeptide from a second disease state or
 CC infectious agent, obtaining a homologue of the antigenic polypeptide or
 CC a nucleic acid encoding an antigenic polypeptide from a second disease
 CC state or infectious agent for the first disease state/infectious
 CC agent, and testing the homology to see if it is an antigenic
 CC polypeptide or a nucleic acid encoding an antigenic polypeptide for the
 CC first disease state or infectious agent). The vaccine, antigens and
 CC polynucleotides are useful for inducing a protective immune response in
 CC vertebrate animals against C. psittaci, C. pneumoniae, other species of
 CC Chlamydia, or a non-chlamydia infection. The antigens are also useful for
 CC antibody preparation techniques. Chlamydia species are responsible
 CC for blindness, sexually transmitted disease, community-acquired
 CC pneumonia and act as co-factors in atherosclerotic plaque formation in
 CC coronary heart disease. C. psittaci in particular is a cause of mastitis,
 CC infertility and abortion in cattle. The present sequence is one of the
 CC cloned Chlamydia psittaci genomic DNA fragments of the invention.

XX Sequence 2520 BP; 774 A; 584 C; 490 G; 672 T; 0 other;

Alignment Scores:

Pred. No.:	1,296-103	Length:	2520
Score:	1497.00	Matches:	357
Percent Similarity:	56.21%	Conservative:	132
Best Local Similarity:	41.03%	Mismatches:	321
Query Match:	34.85%	Indels:	60
DB:	25	Gaps:	25

US-09-830-446-27 (1-841) x ABX99183 (1-2520)

QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
 DB 1 ATGAACATCACTCACTGCTTCTTAATTC-----TCGACCTATTTCCTCGAAT 54
 QY 21 LeuLeuGlyAlaAlaThrThrGluGlu-----LeuSerAlaSerAsnSerPheAspGly 38
 DB 55 TCTTTGAGCTCCGCTCAACGACGCTCAACAGCCTTAACCTCCGCTCGATCAATATGA 114
 QY 39 ThrThrSerThrThrSerPheSerSerLeuThrSerAlaThrAspGlyThrAsnTyr 58
 DB 115 AATGTGACCTCTGAGAGGTTCCAGGTAAAGAAAGAACTTCATCA-----GGAAACAACGTAT 168
 QY 59 ValPheLysAspSerValValIleGluAsnValProThrThrGlyGluThrGlnSerThr 78
 DB 169 ACTGTGACGAGCAATGTGTATCTCTTTCAGAGGAAAGATTTCAGGCTTAAAGAAA--- 225
 QY 79 SerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPheSer 98
 DB 226 AGTTGTTTC-----TCAGCTACGATTAACCTTAACCTTCCAGGAAGAGGATATCT 276
 QY 99 PheThrPheSerSerAlaPheAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAla 118
 DB 277 CTTTGGCTTGAATATATTAATTAACGATCAAGCTTAAGCCCGAGCATTAAATGTTCAAGT 336
 QY 119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
 DB 337 CAAGGAAAGAACTTAGGATCTCAGATTTCTTATTTTCAATGTCTTATGCTCCCA 396
 QY 139 SerThrValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuAsp 158
 DB 397 GGC-----ACAACGAGGTTACGAGCTATACAGCTAAAGCAACAACCTTTAAAGAT 450
 QY 159 AsnAspLysThrValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsn 178
 DB 451 AACTTAGTCTGTCTTCCATTAATAAACTGCTCAACAGACAGAGAGGTGGGCTATCCAGTGT 510

QY 179 AlaGlySer-----LeuLysIleAlaAsnLysSerLeuSerPheIleGly 194
 DB 511 AAGAGAAAGCAAGTATGCTGAATTTAAABAAATTAATATCAGATCTGGTTTCTCGAA 570
 QY 195 AsnSerSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGly 214
 DB 571 AACTCTCCACTCTCAAAAGCGGGGCTATTATTAATGATTAATCAACATTCCTTCAGGT 630
 QY 215 GlyGluThrLysPheGlnGlyAsnThrAlaProThrAlaAlaGly---LysGlyGlyAla 233
 DB 631 GGGCTCAATATTTCTTAACAACCTCTGATCCACGCTTCAATCCCTTAAGCGGGAGCT 690
 QY 234 IleAlaIleLeuAsp---SerGlyThrLeuSerIleSerGlyAspIleIle 252
 DB 691 ATTAGCATTAAGATTAATCAATGATGATGATGATGATGATGATGATGATGATGATGAT 750
 QY 253 PheGluGlyAsn-----ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
 DB 751 TTGCATGGGAAACAAATCATCAAACTAGTGTGAAGTTCTACAGTAACAGAAATTC 810
 QY 269 IleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyHisThrIle 288
 DB 811 ATGATCTCGGCACA---GGGAAATTTACAAACCTACGTCTAAAGACGCTTCGGAAT 867
 QY 289 TyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
 DB 868 TTCTTATGACCTCAATTAATCTGCGGAGATCT-----GATGACCTTAACATT 915
 QY 309 AsnSerProAspThrGlyAspAsnLysGlyTyrThrGlyThrIleValPheSerGlyGlu 328
 DB 916 AATTAATAAAAGAACTGTGAT-----TATACAGAAAGATCGCTTCTCAGGTGA 966
 QY 329 LysLeuThrGluAlaGluAlaLysAspGlyLysAspArgThrSerLysLeuLeuGlnAsn 348
 DB 967 AATTAATCCGATTAAGAAAGAAAGCAAGCGGAAACCTAGCTTCACTTCAACCAACC 1026
 QY 349 ValAlaPheLysAsnGlyThrValValIleLysGlyAspValValIleSerAlaAsnGly 368
 DB 1027 ATCACTATTACAGACAGATCTCTTGAATTAAGATGATGATGATGATGATGATGATGAT 1086
 QY 369 PheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu----- 385
 DB 1087 GTAACCGAGAGAGCGGATCTACCTGATCATGATGATGATGATGATGATGATGATGAT 1146
 QY 386 ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
 DB 1147 TCTTCAGGTGAGAAACATACCTTAATTAATTAATTAATTAATTAATTAATTAATTAAT 1206
 QY 406 AsnGly-----LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
 DB 1207 GGGGGGGGGGCTCTCTCTGCTTAATCTGCAACAATAACAGCAAGTCAAGCTTAATCT 1266
 QY 423 IleAspArgProValValLeuAlaIleSerAspGlySerPheTyrGlnAsnGlyPheLeu 442
 DB 1267 ATTAAC---CGTGTCAATCATGATGATGATGATGATGATGATGATGATGATGATGAT 1323
 QY 443 AsnGluAspHisSerLysThrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIle 462
 DB 1324 GCTACGCTTAACCTTTCACAGCAATAGTAGTCAACATTAACGCTAGTACAGTACACAG 1383
 QY 463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTyr 482
 DB 1384 CCAACGATTAATTAACAAATTAATGCTCCCTCACTCACTTAATGCTTAACAGAAATG 1443
 QY 483 ThrIleAsnTyrSerThrAsp-----AspLysLysAlaThrValSerTyrAlaLysGln 500
 DB 1444 ACAAGTAATTTGGGACACCAAGCAAGTCAAAAGCAAGCAAGCAAGCAAGCAAGCAAGT 1503
 QY 501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTyrGlySer 520
 DB 1504 GGCTACTCCCTTAACCAAGAGACCTTAAGACCTTAAGTCCCAATTAATCTTTGGGGGTGA 1563

Score: 1435.50 Matches: 340
Percent Similarity: 51.43% Conservative: 147
Best Local Similarity: 35.90% MisMatches: 335
Query Match: 33.42% Indels: 125
DB: 24 Gaps: 15

US-09-830-446-27 (1-841) x ABJ91241 (1-2787)

QY 1 MetIleLeuProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
DB 1 ATGAAGACTTCGATCTCTGGGTTTATGTTCTCCGCGTTAGCTTTCTCA---TGTCAC 57
QY 21 LeuLeuGlyValAlaIleThrIleGluLeuLeuSerIleSerAsnSerPheAspGlyThrThr 40
DB 58 CTACAGTCACTACGTAACGAGAACTTTATCACTGATGATAGCTTATATGGAATATC 117
QY 41 SerThrThrSerPheSerSerIleThrSerSerIleThrAspGlyThrAsnIleValPhe 60
DB 118 GATTCAAGAACTTTACTCCAAAACCTTCAGCC-----ACACATATATCTCTA 165
QY 61 LysAspSerValValIleGluAsnValProIleThrGlyIleThrGlnSerThrSerCys 80
DB 166 ACAGAGAGATGCTCTTTTACGAG---CTCGAAAAGGCACTCCCTTATGACAGTTGT 222
QY 81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
DB 223 TTTTAAGCA-----ACCAGGACAACTTACCTCTTGCGGGAACGTCATAGCTTAACG 276
QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyValAlaIleGlySerGluAlaIleAsn 120
DB 277 TTTGGCTTTATATAGTCTGACACTCACTGACAGTGTCTCT---GCATCTACACAGCAAT 333
QY 121 LysThrValIleLeuSerGlyPheSerIleLeuSerPheLeuIleSerProIleSerThr 140
DB 334 AAGAACTTACCTCTCAGGGTTTCTTACTAGATTATCTCTCTCTACAGCAAG 393
QY 141 ValIleAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuLeuAspAsnAsp 160
DB 394 GTTACTACAGGTCAAGGACGCTTCTCTCAGCAGAGCGCTTAATTTAGAAATATTCGT 453
QY 161 LysValLeuIleGluAsnAsnPheSerThrGlyAspGlyValAlaIleAsnValIleGly 180
DB 454 AAACCTGATGCTGCGAAATTTTCTACGACAGATGTGAGCTATCAAGAGCGCTCT 513
QY 180 ----- 180
DB 514 TTCCTTTTAACTGCGACTCTGAGATGCTCTTTTATGTAACAATCTTCATCAACAAG 573
QY 180 ----- 180
DB 574 GAGAGCAATTCCTACTACAGAGCGGCTCGCATAGCAATTAACACAGGTATGTTAGA 633
QY 180 ----- 180
DB 634 TTCCTATCTAACATAGCGCTACGTCAGAGCGCTATGATGATGAAGCAGCTGATA 693
QY 180 ----- 180
DB 694 CTATCGAACAAATTTCTATATTGGAAGGAGTACGCGAAACTACTGCGCGTGC 753
QY 181 ----- 181
DB 754 ATCTGCAACACAAAGGAGTATCTCTGAACTGATATCTCTAACATTAAGACTCTG 813
QY 191 SerPheIleGlyAsnSerSerThrArgGlyValAlaIleIleThrIleAsnLeuThr 210
DB 814 ATCTTGCTTCAACAGTACGAGAAACAGCGGTGCGCCCATTCATGCTAAAGACTGACC 873
QY 211 LeuSerSerGlyGlyIleThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
DB 874 CTATTCCTGAGGCTTTACAGAGTTCTACGAAATATATCTTCATACGACACTCTTAC 933
QY 231 GlyGlyValAlaIleAlaIleAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250

DB 934 GGGGGTGTATCAGCATTCATGCTCAGAGAGCTCAGCTTCTTCAGAGACAGCAAGAAC 993
QY 251 IleIlePheGluGlyAsnThrIle-----GlyAlaThrGlyThrValSerIleSer 267
DB 994 ATTACCTTTGTAAAGAAATACCTTACACACACCGGAATCCGATCTCTTAAACGTAAAT 1053
QY 268 AlaIleAspLeuGlyThrSerAlaIleThrAlaIleAsnArgAlaIleGlnIleIleThr 287
DB 1054 GCGATCAACATAGAGATGAAACGGAATTCACGGAATTCAGGCTCTTAAATCTATCA 1113
QY 288 IleThrPheThrAspProIleThrValIleThrGlySerThrSerValAlaAspAlaLeuAsn 307
DB 1114 ATTCTCTCATGATCCCATCACTTCAAGAGAACTCATCA-----GACGATTTGAAG 1167
QY 308 IleAsnSerProAspThrGlyAspAsnIleGlyIleThrGlyThrIleValPheSerGly 327
DB 1168 ATAAATTAACGGCTCTCGGAGCTCTCAATCCATATCAAGAAACGATTCATTTTCTGGA 1227
QY 328 GluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerIleLeuGln 347
DB 1228 GAACCTTACACAGCATGAACTTAAGTTGCTGACAAATTTAAATCTTCATTCACGACG 1287
QY 348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
DB 1288 CCACTCTCCCTATCCGAGAGAAAGTATTTGCTACAAAGAGACTCTTACAGACACG 1347
QY 368 GlyPheSerGluAspAlaAsnSerIleLeuIleMetAspLeuGlyThrSerLeuValAla 387
DB 1348 AGCTCTCTCAAGAGCGGTTCTCTCCGCGATGATTCAGGAACGACATTAATCACT 1407
QY 388 AsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGly 407
DB 1408 ACAGCTGGAGATTTTCAATCAGACCTTAGCAATCAAGTTACTCTTAGGCTTTAAG 1467
QY 408 LysLysIleLysLeuSerAlaIleThrAlaGlnLysAspIleArgIleAspArgProVal 427
DB 1468 CAGCCGTCAGCTTACACAAAGAGTCTTCAATTAAGATGATCTGATCTGGAGACTC 1527
QY 428 ValLeuAlaIleSerAspGluSerPheIleGlnAsnGlyPheLeuAsnGluAspPheSer 447
DB 1528 AACCTATTGATATTAAGAGAACTATTATGAAGCATATGTTCCAGCATGACGACTC 1587
QY 448 TyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
DB 1588 TTC---TCTCTATTAAATAATCACGGTTGATGCTGATGTTGATCTAACGTTGACATCAGC 1644
QY 468 SerIleAspAlaVal-----GlnSerProIleGlyIleGlnIleLysIle 482
DB 1645 AGCTTATCCCTGTTCTCTGCTGAGATCTTAATTCAGAAATAGGATTCACAGACATAGG 1704
QY 483 ThrIleAsnTrpSerThrAsp-----AspLysLysAlaThrValSerTrpAla 498
DB 1705 AATGTTAATTTGACCTACGATACAGTACCAATATCAAAAGAGCCACGCGAACTTGAGCC 1764
QY 499 LysGlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrp 518
DB 1765 AAAACAGAAATTTGTTCCAGCCCGAAAGAAATTCGGCTTATAGCAATACCTTAGG 1824
QY 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
DB 1825 GAGGCTTACTAGACATTCGCTCTCGCAACAGCTTGTAAGATCGCGCGCAACTGGATAG 1884
QY 539 ProIleGluLysArgPheTrpValAlaGlyIleSerAsnValLeuIleAsnSerGlyArg 558
DB 1885 GAACACAAACAAAGTTTCTGGGTTCTCTCCATGACCAACCTCTCTGATATAGACTGAGAT 1944
QY 559 GluAsnGluArgLysPheArgIleValSerGlyValAlaValAlaGlyLysSerThrArg 578
DB 1945 GAATATCGAAAGCTTCCGTCATACCTCTGAGAGCTACGTCATCGGTGAAAGTCTCAC 2004
QY 579 MetProGlyLysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598

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Db      2005 ACTCCATAAGACGACCTATTACCTTGGCGTTCGCCATCTCTTGTCTAGACAAAGAT 2064
QY      599 TyrPheMetAenThrAsnPheAlaIyThrThyAlaGlySerLeuArgLeuGlnHisAap 618
Db      2065 TGTTTATCGCTCACACAACTTAGAACCTAGACGGTAACTTATTTCTTCAAGCACTCT 2124
QY      619 AlaSerLeuTySerValValSerIleLeuLeuGlyGlyGlyLeuArgGlyIleLeu 638
Db      2125 CATACCTTACAAACCCAAACATTTAGATTAGAGAAAGCAAAATTTTCTGAATCAGCT 2184
QY      639 LeuProTyValSerIyThrLeuProCySerPheTyGlyGlyLeuSerTyGlyHis 658
Db      2185 ATAGAAAAATTCCTGAGGAAATTCCTCCAGCTTGAATGTCCAAATGTTCTGTCAGCCAT 2244
QY      659 ThrAspHisArgMetLeuThrGlu-----SerLeuProProProProProThrLeuSer 676
Db      2245 TCAGACAAACCGTATGAAAGCACTATACCTCATTCGCA----- 2283
QY      677 ThrAspHisIleThrSerTyPheGlyTyValTTPAlaGlyLeuGlyThrArgValAla 696
Db      2284 GAATCCGAAGTTCCTTGGAGCAACAGGTATAGCTGGTGGTATGCGGCTAGACCTTCT 2343
QY      697 ValGluAenThrSerGlyValGlyPhePheGlnGlyTyThrProPheValIyValGln 716
Db      2344 TTGTGTTCTTCCAAACCATCTCTTTCAGAACCTTCATTCACAGATGAAGTCGAA 2403
QY      717 AlaValTyAlaIleArgIleAspSerPheValGlyLeuGlyAlaIleSerArgAspSer 736
Db      2404 ATGTTTATGATATCAACAAATAGCTTTCGAAAGCTTAGAGATGCGCGTGTATAGT 2463
QY      737 AspSerHisIleTyArgLeuAlaIleProLeuGlyIleIyLe-----LeuGlyIyAspPhe 755
Db      2464 ATTTGAGAGCTGCTTAACTCTCGATTCCTGTGGGCGGCAAAATGTCGACGGGCAATTC 2523
QY      756 AlaGlnGlnTy--TyHisValValAlaMetTySerProAspValCysArgSerAsn 774
Db      2524 GGAGATCTTACACCATATGATCTCTCAGAGATCTTGTTCGCAATGTCTATGTAAACAT 2583
QY      775 ProIyAsyThrThrThrLeuSerAsnGlnGlySerThyIyThrIyPheGlySerAsn 794
Db      2584 CCCCAATCTTACAGCGCTCTGTGATGACCCCAAGACTCTTGAATAATTCGCGGTGCAT 2643
QY      795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
Db      2644 CTTTCAAGACAGGCAATTTTACAGAGGGTATGCAACAACGTCACAACTCCAAATGCT 2703
QY      815 GluLeuPheGlyAsnDheGlyPheGlyTyPArgGlySerSerArgSerTyArgValAap 834
Db      2704 GAGCTCTTCCGACATTAACCTATGAACTCCGTGATCTTCAAGAACTACAAATGTATAGT 2763
QY      835 AlaGlySerTyIleLeuAspPhe 841
Db      2764 GTTGTACCAAACTCCGATTC 2784

RESULT 13
AAA30847
ID      AAA30847 standard; DNA; 2950 BP.
AC      AAA30847;
DT      29-AUG-2000 (first entry)
DB      Chlamydia antigen CPN100634 full length coding sequence.
XX      Chlamydia antigen; diagnosis; infection; community acquired pneumonia;
XX      therapy; upper respiratory tract disease; bronchitis; sinusitis;
XX      asthmatic bronchitis; adult-onset asthma; acute exacerbations of asthma;
XX      da.
XX      Chlamydia pneumoniae.
XX      Key Location/Qualifiers
XX      CDS 101..2887

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FT      /*tag= a
FT      /product= Chlamydia antigen CPN100634
XX      MO200032794-A2.
XX      08-JUN-2000.
PD      01-DEC-1999; 99WO-CA01147.
XX      01-DEC-1998; 98US-0110339.
PR      01-DEC-1998; 98US-0110340.
PR      01-DEC-1998; 98US-0110427.
PR      01-DEC-1998; 98US-0110428.
PR      01-DEC-1998; 98US-0110438.
XX      (CONN-) CONNAUGHT LAB LTD.
XX      Murdin AD, Oomen RP, Wang J;
PI      WPI; 2000-412339/35.
XX      P-PEDB; AAY90236.
DR      Nucleic acids encoding polypeptide antigens from Chlamydia useful for
PT      preventing, diagnosing and treating diseases such as community acquired
PT      pneumonia, bronchitis, sinusitis and asthmatic bronchitis, adult-onset
PT      asthma -
XX      Claim 2, Fig 1, 17app, English.
XX      This sequence encodes a Chlamydia antigen of the invention, designated
XX      CPN100634. The nucleic acids (and their complementary sequences) may be
XX      used as diagnostic agents for detecting the presence of nucleic acids
XX      encoding Chlamydia antigens in samples according to standard methods,
XX      and therefore, for diagnosing Chlamydia infections. For example, they may
XX      be used as primers and probes for diagnostic polymerase chain reaction
XX      (PCR) assays. Antisense sequences may be used to down regulate
XX      expression of the proteins and may be used to treat infections. The
XX      nucleic acids may also be used to produce the protein antigens they
XX      encode according to standard recombinant DNA methodologies. The
XX      proteins may then be used as antigens for the production of antibodies
XX      (i.e. as vaccines) for preventing infection by Chlamydia. The
XX      antibodies may also be used as diagnostic reagents for detecting
XX      CC infections. Chlamydia is a pathogen implicated in the development of
XX      (for example) community acquired pneumonia, upper respiratory tract
XX      disease (especially bronchitis and sinusitis, asthmatic bronchitis,
XX      adult-onset asthma and acute exacerbations of asthma in adults.
XX      6Q Sequence 2950 BP; 851 A; 670 C; 596 G; 833 T; 0 other;
XX      Alignment Scores:
XX      Pred. No.: 7,02e-99 Length: 2950
XX      Score: 1435.50 Matches: 340
XX      Percent Similarity: 51.43% Conservative: 147
XX      Best Local Similarity: 35.90% Mismatches: 335
XX      Query Match: 33.42% Indels: 125
XX      DB: 21 Gaps: 15
XX      US-09-830-446-27 (1-841) x AAA30847 (1-2950)
QY      1 MetIyIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db      101 ATGAGAGACTTGATTCCTGGGTTTAACTTCTCCGTTGATGCTTTCCA---TGTCA 157
QY      21 LeuLeuGlyAlaAlaIleThrThrGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db      158 CTACAGTCACTAGACGAGAACTTTATCACTGATGATAGCTTTATATGAAATATTC 217
QY      41 SerThrThrSerPheSerSerTyThrSerSerAlaThrAspGlyThrAsnTyValPhe 60
Db      218 GATTCAGAACTTATCTCCAAAACCTTCAGCC-----ACAACATATTCCTCA 265
QY      61 TyAspSerValValIleGluAenValProIyThrGlyIyThrGlnSerThySerCys 80

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Db 266 ACAGGAGATGCTCTTTACGAG---CTGGAAAGGCACTCCCTATCTGACAGTTGT 322
 Qy 81 PhelysenaApAlaAlaIaGlyAspLeuAsnPhelLeuGlyGlyPheSerPheThr 100
 Db 323 TTTAAGAA-----ACCAGGACAATCTTACCTCTTGGGAAAGGTCACTAGCTTAAG 376
 Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
 Db 377 TTGGCTTTATAGATGCTGACACTCATGACAGTGCTCT---GCATCTACACAGCAAT 433
 Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuSerProAlaSerThr 140
 Db 434 AAGAAATTAACCTCTTCAGGGTTCCTTACTGAGTTTATTCCTCTCTACACAAAG 493
 Qy 141 ValThrAsnGlyLeuGlyAlaAlaIleAsnValLysGlyAsnLeuSerLeuAspAsnAsp 160
 Db 494 GTTACTACAGGTACGAGGAACGCTTCTCTGACGAGAGGCGTAATTGAAATTTATTCGT 553
 Qy 161 LysValleuIleGlnAspAsnPheserThrGlyAspGlyAlaAlaIleAsnCybalagly 180
 Db 554 AAACCTGATGCTGCGAATTTTCTACTGACAGATGTGAGCTATCAAGAGGCTCT 613
 Qy 180 ----- 180
 Db 614 TTCCTTTAACTGACACTTCTGAGATGCTCTTTTATGTAACAACCTTCATCAACAAG 673
 Qy 180 ----- 180
 Db 674 GAGAGACAATTCCTACTACAGACAGGCGCTCGCATAGCAATTAACACAGGTTATGTTAGA 733
 Qy 180 ----- 180
 Db 734 TTCCTATCTAACAATAGCGTCTAGCGTACAGAGGCGCTATGATGATGAAGCAGCTGATA 793
 Qy 180 ----- 180
 Db 794 CTATCGAACAACAATTTCTATATTTGAAAGGAAATGACAGCAAACTACTGCGCGTGC 853
 Qy 181 ----- SerLeuLysIleAlaAsnLysSerLeu 190
 Db 854 ATCTGCAACACCAAGGAGATGATCTCTGAACTGATTAATCTCTAACAATTAAGACTCTG 913
 Qy 191 SerPheIleGlyAsnSerSerThrArgGlyGlyAlaIleIleThrLysAsnLeuThr 210
 Db 914 ATCTTGCTTCAACACGTAAGCAAGAAACAGGCGGTGCGCATCATGCTAATAAAGCTAGCC 973
 Qy 211 LeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLys 230
 Db 974 CTTCCTCTGAGGCTTTACAGAGTTCCTACGAATATGCTCATACGCAACTCCCTAAG 1033
 Qy 231 GlyValAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
 Db 1034 GGGGGGTCTATGACGATCATGCTCTGAGAGCTGCTCTTCTGCAAGACAGCAAAAC 1093
 Qy 251 IleIlePheGlnGlyAsnThrIle-----GlyAlaThrGlyThrValSerIleSer 267
 Db 1094 ATTACCTTTAGTAAGAAATACCTTTACAACAACAGGAGATCCGATCTCTTAACGTAA 1153
 Qy 268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaAlaGlnGlyIleThr 287
 Db 1154 GCATCAACATACGAAAGTAACGGAAATTCACGGAATTACGGCTGCTAATAAATCTATAC 1213
 Qy 288 IleTyrPheTyrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
 Db 1214 ATTTCTCTTAATATCCATCACTTCAGAAAGAACTCATCA-----GACGTATTAAGAG 1267
 Qy 308 IleAsnSerProAspThrGlyAspAsnLysGlyTyrThrGlyThrIleValIlePheSerGly 327
 Db 1268 ATAAATTAACGCTCTGCGGAGGCTCAATCATCATCAAGAAAGCAATTTCTTCTGAG 1327
 Qy 328 GluLysLeuThrGluAlaGlyAlaLysAspGluLysAsnArgThrSerLysLeuLeuGln 347
 Db 1328 GAACCTCAACAGCAGATGAATTAAGTTGACAGCAATTAATAATCTTCATTCACGACAG 1387

Qy 348 AsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsn 367
 Db 1388 CCAAGTCTCCCTATCCGAGAGAAAGTTATGTCTACAAAGAGGACTCATTTAGAGACAGC 1447
 Qy 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAla 387
 Db 1448 AGCTTCTCAAGAGCCGCTTCTCTCCGCGATGATTCAGGAAGCAATTAATCAACT 1507
 Qy 388 AsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArgAsnGly 407
 Db 1508 ACAGCTGGAGATTAATCAATCAAGAACTTAGGAATAAATGACTCTTAGGCTTTAAG 1567
 Qy 408 LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
 Db 1568 CAGCCGCTACGCTTACACCAAAAGGTGCTTCAAAATAAGTATGCTATCTGGAGAGCTC 1627
 Qy 428 ValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGluAspHisSer 447
 Db 1628 AACCTGATTAATTAAGAGGAACATTTATGAAGATCATATGTTACAGCATGACCATC 1687
 Qy 448 TyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
 Db 1688 TTC---TCTCTATTAATAATCAAGGTGATGCTGATGTTGATATCACTTGAACATCAC 1744
 Qy 468 SerIleAspAlaVal-----GlnSerProTyrGlyTyrGlnGlyLysTP 482
 Db 1745 AGCTTATCCCTGTTCTCTGCTAGATGCTCTAATTCGAATACGGAATTCACAGACATAG 1804
 Qy 483 ThrIleAsnTyrSerThrAsp-----AspLysLysAlaThrValSerTyrAla 498
 Db 1805 AATGTTAATTTGACATACGATACAGTACCAAAATACAAAGAGCCACGGCAATCTGAGCC 1864
 Qy 499 LysGlnSerPheAsnProThrAlaGlnGlnAlaProLeuValProAsnLeuLeuTyrP 518
 Db 1865 AAAACAGATTTGTTCCAGCCCGAAGAAATATGCGTTGATGACATACCTATAG 1924
 Qy 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAla 538
 Db 1925 GAGATCTTACGACATTCGCTCTCTGCAACAGCTTTGAGATGCGGCCCACTGATAG 1984
 Qy 539 ProTyrGluLysArgPheThrValAlaGlyIleSerAsnValLeuHisArgSerGlyArg 558
 Db 1985 GAACACAAACAAAGTTTCTGGGTTCTCTGATGACGAACCTTCCTGATTAAGCTGAGAT 2044
 Qy 559 GluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValAlaGlyAlaSerThrArg 578
 Db 2045 GAAATACGAAAGGCTTCGTCATACCTCTGAGAGCTAGCTACGCTGGAAGTGTCTAC 2104
 Qy 579 MetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598
 Db 2105 ACTCTTAAGACGACCTATTTACCTTGGCTTCTGCACTCTCTTCTGAGACAAAGAT 2164
 Qy 599 TyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuHisAsp 618
 Db 2165 TGTTTATGCTCAACAACAACCTTAAGACTTAAGGAACTTAATTTCTCAAGACCTCT 2224
 Qy 619 AlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyGlyLysLeuArgGluIleLeu 638
 Db 2225 CATACCTCAACACCCCAAAACTATTTAGATTAAGAAAGCAAAAGTTTCTGAATCAGCT 2284
 Qy 639 LeuProTyrValSerLysThrLeuProCysSerPheTyrGlyLysLeuSerTyrGlyHis 658
 Db 2285 ATAGAAAATTCCTCAAGGAAATTCCTCAAGCTTGAATGATGCAAGTTCTGTTACCAT 2344
 Qy 659 ThrAspHisArgMetLysThrGlu-----SerLeuProProProProThrLeuSer 676
 Db 2345 TCAGACAACCGTATGAAACGACATTAACCTCATTTGCA----- 2383
 Qy 677 ThrAspHisThrSerTyrGlyGlyTyrValTyrAlaGlyGluLeuGlyThrArgValAla 696
 Db 2384 GAATCGAAGGTTCTTGGAGCAACAGATGATAGCTGTGATGCGCTAGACCTTCTCT 2443

QY 697 ValGluAenThrSerGlyArgGlyPhePheGlnGlyThrProPheValIleValGln 716
 DB 2444 TTGTTCTTCCACACCATCTCTTTTCAAGACCTTCATCCACAGATGAATCCAA 2503
 QY 717 AlaValIleAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
 DB 2504 ATGGTTTATGATACCAAAATAGCTTCTTCGAAACCTCAGAGATGAGCCGCTTTTGT 2563
 QY 727 AspSerIleLeuTyAsnLeuAlaIleProLeuGlyIleLeu---LeuGluIleArgPhe 755
 DB 2564 ATTTGAAGAGCTCTTAACCTCTCGATCTCTGTGGGGCGAAATTCGTGAGGGGATATC 2623
 QY 756 AlaGlnGlyIle---TyrlIleValAlaIleMetTySerProAspValCysArgSerAsn 774
 DB 2624 CGAATTCCTACACCTATGATCTCAGAGATCTTTGTTTCCGATGCTATCTAACAAT 2683
 QY 775 ProGlyCysThrThrThleuLeuSerAsnGlnGlySerTrpIleThrIleGlySerAsn 794
 DB 2684 CCCCATCTACAGCGACTCTGTGTGATGAGCCGACGCTCTTGAAATTCGCGGTGCAAT 2743
 QY 795 LeuAlaATGAlaIleGlyIleValGlnAlaIleSerGlyPheArgSerLeuGlyAlaIleAla 814
 DB 2744 CTTTCAAGACAGCGACTTTTACTGAGGGGTAGCAACACTACCTACACTCCAAATGT 2803
 QY 815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyAsnValAsp 834
 DB 2804 GAGCTCTTCGACATTAAGCTATGAACTCCGTGATCTTCAAGAACTACAAATGAT 2863
 QY 835 AlaGlySerIleGlyIlePhe 841
 DB 2864 GTTGGTACCMAACTCCGATTC 2884
 RESULT 14
 AAX06816
 ID AAX06816 Standard; DNA, 3200 BP.
 AC AAX06816;
 XX
 DT 26-APR-1999 (first entry)
 DE Chlamydia pneumoniae surface exposed protein Omp4 DNA.
 XX
 KM Omp4; outer membrane protein 4; surface exposed protein; antigen;
 XX infection; diagnosis; vaccine; atherosclerosis; asthma; ss.
 OS Chlamydia pneumoniae.
 XX
 FH Key Location/Qualifiers
 FT CDS 205..2991
 FT /*tag= a
 PN MO9858953-A2.
 XX
 PD 30-DEC-1998.
 XX
 PF 19-JUN-1998; 98WO-DK00266.
 XX
 PR 23-JUN-1997; 97DK-0000744.
 XX
 PA (BIRK/) BIRKELUND S.
 XX (CHRI/) CHRISTIANSEN G.
 XX
 PI Birkelund S, Christiansen G, Knudsen K, Madsen A;
 XX Mygind P;
 DR MPI; 1999-105610/09.
 DR P-PSDB; AAM88417.
 XX
 XX Species-specific test for identifying mammae infected with
 PT Chlamydia pneumoniae - comprises detecting antibodies specific for
 PT outer membrane proteins of C. pneumoniae or nucleic acids encoding
 PT these proteins
 XX

PS Claim 6; Page 35-40; 115pp; English.
 XX
 CC This DNA sequence codes for the novel 98.9 kDa surface exposed
 CC protein Omp4 (see AAM88417) of the human respiratory pathogen
 CC Chlamydia pneumoniae. By generating antibodies against C.
 CC pneumoniae outer membrane complex, a polyclonal antibody (PAB 150)
 CC was obtained which reacted with outer membrane proteins. The
 CC antibody was used to identify the genes (see AAX06816-27) encoding
 CC Omp4-Omp5 proteins (see AAM88417-28) in an expression library of
 CC C. pneumoniae DNA. The genes are situated in 2 gene clusters:
 CC Omp2,11,10,5,4,13 and 14 in one cluster and Omp6,7,8,9 and 15 in
 CC the other; and encode polypeptides of about 89.6-100.3 kDa and
 CC about 56.1 kDa. The invention provides a new species specific test
 CC for identifying mammae (including humans) infected with Chlamydia
 CC pneumoniae. The test comprises detecting antibodies specific for
 CC Omp4-Omp5 or detecting nucleic acid fragments encoding these outer
 CC membrane proteins, especially by PCR. The proteins are also used
 CC in the diagnosis of C. pneumoniae infection in mammals. The
 CC nucleic acids and proteins can also be used in the immunization of
 CC mammals, the nucleic acids being particularly useful as DNA
 CC vaccines for effecting in vivo expression of antigens. The
 CC vaccines may also prevent atherosclerosis and bronchial asthma,
 CC which are possibly associated with C. pneumoniae.
 XX
 SQ Sequence 3200 BP; 946 A; 708 C; 623 G; 923 T; 0 other;
 Alignment Scores:
 Pred. No.: 7,786-99 Length: 3200
 Score: 1435.50 Matches: 340
 Percent Similarity: 51.43% Conservative: 147
 Best Local Similarity: 35.90% Mismatches: 335
 Query Match: 33.42% Indels: 125
 DB: 20 Gaps: 15
 US-09-830-446-27 (1-841) x AAX06816 (1-3200)
 QY 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
 DB 205 ATGAAGACTTGATCCCTGCGTTTGGTTTCCCGGTAGCTTCTCA---TGTCAC 261
 QY 21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThr 40
 DB 262 CTACAGTCACCTAGCTTAACGAGAACTTTATACCTGATGATACCTTAAAGAAATATC 321
 QY 41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAsnTyValPhe 60
 DB 322 GATTCAGAACGTTTACTCCAAAACCTTCAGCC-----ACAACTATTCCTA 369
 QY 61 LysAspSerValIleGluAsnValProLysThrGlyIleThrGlnSerThrSerCys 80
 DB 370 ACAGAGATGCTCTTCTTACGAG---CTGAAAGAGCACTCCCTATCTGACAGTTGT 426
 QY 81 PheLysAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
 DB 427 TTTAAGCAA-----ACCACGACAACTTACCTTCTGGGAAACGTCATATGTAACG 480
 QY 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAsn 120
 DB 481 TTGGCTTATAGATGCTGCGACTCATGACAGGTCTCT---GCATCTACACAGCAAT 537
 QY 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
 DB 538 AAGATCTTACCTTCTGAGGTTTCTTCTTACTGATGTTTGAATCCTCTTACGCAACG 597
 QY 141 ValThrAsnGlyLeuGlyAlaIleAsnValIleAsnValIleAsnSerLeuLeuAspAsp 160
 DB 598 GTTACTACAGCTCAGGAGAACGCTTCTCAGACAGAGAGCGTAATTTAGAAATATTCGT 657
 QY 161 LysValIleuIleGluAsnAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
 DB 658 AAACCTGATGTTGCTGGAAATTTTCTACTGCAATGTGAGCTATCAAGAGCGCTCT 717
 QY 180 ----- 180

Db 718 TTCCTTTAATGGCACTTGTGAGATGCTTTTAAAGAACACTTCATCAACAAG 777
 QY 180 ----- 180
 Db 778 GGAGGCAATTGCTACTACAGCAGCGCTCGCATAGCAATMACAGGTTATGTTAGA 837
 QY 180 ----- 180
 Db 838 TTCCTATCAACATAGCGTCTACGTACAGAGCGCTATGATGATGAAGCAGCTGATA 897
 QY 180 ----- 180
 Db 898 CTATGCAACAACAATTCTATATTTGAAGGAGATGACGAAACTACTGCGCGTGG 957
 QY 181 ----- SerLeuLys11eal1aAenLysSerLeu 190
 Db 958 ATCTGCACACCAAGCGAGTGATCTCTGAACATGATATCTCTAACATTAAGACTTG 1017
 QY 191 SerPhe11eal1aAenLysSerLeu190 210
 Db 1018 ATCTTGTCTTCAACAGTACGAGAAACAGCGGTGCGCATCTCAATCTTAAAGCTAGCC 1077
 QY 211 LeuSerSerGly1ygl1uThrLeuPheGlnGlyAsnThrAlaProThrAla1aGlyLys 230
 Db 1078 CTTTCTCTGAGAGCTTTACAGAGTTTCAAGAAATATGTCATCAGCACTCCTTAAG 1137
 QY 231 Gly1yAla11eal1aAenSerGly1yThrLeuSer11eSerGly1yAsp 250
 Db 1138 GGGGGGTCTATCGATCGCTCAGAGAGCTCAGTCTTCTGACAGACAGAAAC 1197
 QY 251 11e11ePheGlnGlyAsnThr11e-----GlyAlaThrGly1yThrAlaSerHisSer 267
 Db 1198 ATTACCTTGTAAAGATACCTTACCAACACCGGAAGTACGATCTCTTAAACGTAAAT 1257
 QY 268 Ala11eAspLeuGly1yThrSerAlaLys11eThrAlaLeuArgAla1aGlnGlyHisThr 287
 Db 1258 GCGATCAACATAGGAAGTACCGGAATTCACCGAATTACGGCTCTTAAATCTATACA 1317
 QY 288 11eTyPheTyAspPro11eThrVal1yThy1ySerThrSerVal1aAenAlaLeuAen 307
 Db 1318 ATTTCTTATATATCCATCACTTCAAGAAAGAACTCATCA-----GACGTAATTAAG 1371
 QY 308 11eAsnSerProAspThrGly1yAspAenLysGly1yThy1yThy1yThr11eVal1yPheSerGly 327
 Db 1372 ATTAATTAACGGCTCTCGGAGGCTCTCAATCCATTCATCAAGAAAGATCTTATTTCTGA 1431
 QY 328 GlnLysLeuThrGln1aGlnAlaLysAspGlnLysAsnArgThrSerLysLeuLeuGln 347
 Db 1432 GAACCTTAACAGCAATGAACTTAAAGTTGCTGACAAATTTAAATCTTCAATTCACGCA 1491
 QY 348 AsnVal1aAenLys1yThrVal1yVal1yLeuLysGly1yAspVal1aLeuSerAlaAen 367
 Db 1492 CCAAGTCTCCCTATCCGAGGAAGTATATGCTCAAAAGGAGTCACTTAAAGACAG 1551
 QY 368 GlyPheSerGlnAspAlaAenSerLysLeu11eMetAspLeuGly1yThrSerLeuVal1a 387
 Db 1552 AGCTTCTTCACAAAGCGGTCTCTCTCGCATGATTCAGAAAGCATATATCAACT 1611
 QY 388 AsnThrGlnSer11eGlnLeuThrAsnLeuGln11aAen11eAspSerLeuArgAsnGly 407
 Db 1612 ACAGCTGGAGATTTACATCAACAACTTGAATGATGATGATGATGATGATGATGATGAT 1671
 QY 408 LysLys11eLysLeuSerAla1aThrAlaGlnLysAsp11eArg11eAspArgProVal 427
 Db 1672 CAGCCCTTACAGCTTACAGCAAAAGGCTTCAATTAAGTATCGATCTGGAAGCT 1731
 QY 428 ValLeuAla11eSerArgLysSerPheTy1yGlnAsnGly1yPheLeuGlnLysAspHisSer 447
 Db 1732 AACCTATGATATGTAAGGAACATTTATGAAGATCATATGTTCCAGCCATGACAGCTC 1791
 QY 448 TyAspGly1yLeuGlnLeuAspAlaGly1yAsp11eVal11eSerAlaAenSerArg 467

Db 1792 TTC---TCTCTATTAATAATCAAGGTTGATGCTGATGTTGATACATACGTTACATCAGC 1848
 QY 468 Ser11eAspAlaVal1-----GlnSerProTy1yGly1yThy1yGlnGly1yThy1y 482
 Db 1849 AGCTTATCCCTGTTCTGCTGAGATCTTAATTAATGAAATAGACATTCAGAGACATAG 1908
 QY 483 Thr11eAsnThrSerThrAsp-----AspLysVal1aThrVal1ySerThrAla 498
 Db 1909 AATGTTATGACATACGATACAGTACCAATTAACAAAGAGCCACGCACTTGAGACC 1968
 QY 499 LysGlnSerPheAsnProThrAlaGlnGlnGlnAlaProLeuVal1yProAsnLeuLeuTrp 518
 Db 1969 AAAACAGATTTGTTCCAGCCCCCAAAATATGCGTTATGATGATGATGATGATGATGATG 2028
 QY 519 GlySerPhe11eAspVal1ySerPheGlnAsnPhe11eGlnLeuGly1yThy1yGlnGlyAla 538
 Db 2029 GAGATCTTACTGACATTCGCTCTGCAACAGCTTGTAGATGAGCGGCAACTGATATG 2088
 QY 539 ProTy1yGlnLysArgPheThrVal1aGly1yLeuSerAsnVal1eHisArgSerGlyArg 558
 Db 2089 GAACACAAACAGGTTCTCGGTTCTCCCATGACAGAACTTCTGCTATAGACTGAGAT 2148
 QY 559 GlnAsnGlnArgLysPheAsnArgHisVal1ySerGly1yAlaVal1yGlyAla1ySerThrArg 578
 Db 2149 GAAATTCGCAAGGCTTCGCTCATACCTCGAGGCTACGTCATCGTGGAAGTCTCAC 2208
 QY 579 MetProGly1yAspThrLeuSerLeuGly1yPheAlaGlnLeuPheAlaArgAspLysAsp 598
 Db 2209 ACTCTTAAAGACACTTATTAATCTTGGGTTCTGCCATCTCTTGTGAGAACAAAGAT 2268
 QY 599 TyPheMetAsnThrAspPheAlaLysThrTy1yAlaGly1ySerLeuArgLeuGlnHisAsp 618
 Db 2268 TGTTTATGCTCACAAACACTCTAGAACTTACGAGTGAACCTTATCTTCAAGACACTCT 2328
 QY 619 AlaSerLeuTy1ySerVal1ySer11eLeuLeuGlnGly1yGly1yLeuArgGlnLeu 638
 Db 2329 CATACCTTCAACCCCAAAATTAATGATTAAGTAGAAGACAAAGTTTCTGAATCAGCT 2388
 QY 639 LeuProTy1yVal1ySerLysThrLeuProCysSerPheTy1yGly1yGlnLeuSerTy1yHis 658
 Db 2389 ATAGAAAATTCCTAGGAAATTCCTCCATGAGTTCGATTCGATTCGATTCGATTCGATTC 2448
 QY 659 ThrAspHisArgMetLysThrGln-----SerLeuProProProProProProProPro 2487
 Db 2449 TCAGACACCGTATGGAACGCACTATACCTATGCCA----- 2487
 QY 677 ThrAspHisThrSerTy1yGly1yTy1yVal1yTrrAlaGly1yGlnLeuGly1yThy1yVal1a 696
 Db 2488 GAATCGAAGGTTCTTGGAGCAACAGGTATAGCTGGTGGTATGAGGCTTACAGCTTCTCT 2547
 QY 697 Val1yGlnAsnThrSerGly1yArgGly1yPhePheGlnGly1yThy1yProPheVal1yVal1yGln 716
 Db 2548 TTTGTTCTTCCCAACCCACATCTCTTTCACAGACCTTCATTCACAGATGAAAGTCGAA 2607
 QY 717 AlaVal1yTrrAlaArgGlnAspSerPheVal1yGlnLeuGly1yAla11eSerArgAspPheSer 736
 Db 2608 ATGTTATATGATCAACAAATATGCTTTCGAAAGCTCTAGAGATGCGCTGTTTAT 2667
 QY 737 AspSerHisLeuTy1yAsnLeuAla11eProLeuGly1yLeu1yLeuGlnLysArgPhe 755
 Db 2668 ATTTGAGAGGCTCTTAACCTCGATTCCTGCGGTGCGAAATTTGTCAGAGGGGATATC 2727
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 Db 2788 CCCCATCTACAGCACTTGTGATGAGCCAGACTCTTGAAGAAATTCGCGGTGCAAT 2847
 QY 795 LeuAlaArgGlnAlaGly1yLeuAlaGlnAlaSerGly1yPheArgSerLeuGly1yAla1aAla 814
 Db 2848 CTTTCAAGACAGCACTTTTACTGAGGGGTACCAACACTAGCTTACAACTCCAACTTGT 2907

Qy	815	GlueuphegiyaamphgilyphedutripargjlyserSerArgSerTyramValasp	834
Db	2308	GAGCTCTTCGACATTAAGCGATAGAACTCCCTGCACTTCAAGAACTACATTAAT	2965
Qy	835	AlaGlySerTygIleLeuPhe' 841	
Db	2368	GTTGTACCAAACTCCGATTC	2988
RESULT 15			
ID	AAc81914/c		
AC	AAc81914	standard; DNA; 273254 BP.	
XX	AAc81914;		
DT	27-FEB-2001	(first entry)	
DB	Chlamydia pneumoniae genome DNA.		
KM	Genome; diagnosis; vaccine; ds.		
XX	Chlamydia pneumoniae.		
XX	MO200027994-A2.		
PN	18-MAY-2000.		
PD	12-NOV-1999;	99MO-US26923.	
PF	12-NOV-1998;	98US-0108279.	
PR	08-APR-1999;	99US-0128606.	
XX	(REGC) UNIV CALIFORNIA.		
PA	Stephen R, Mitchell W, Kalman S, Davis R;		
PI	WPI: 2000-376516/32.		
DR	Isolated nucleic acid for use in diagnostic and analytical methods		
PT	encodes genomic sequence of Chlamydia pneumoniae -		
XX	Claim 2; Page 128-320; 320pp; English.		
PS	This invention describes a novel nucleic acid (N1) encoding a Chlamydia		
XX	pneumoniae protein (P1), given in the specification. The isolated nucleic		
CC	acid is useful for diagnostic and analytical methods, such as,		
CC	hybridization-based assays or amplification-based assays. The protein may		
CC	be used for diagnostic purposes, for their enzymatic or structural		
CC	activity, or as a vaccine. The invention also describes (1) a probe		
CC	comprising a hybridizing fragment of N1; (2) an isolated nucleic acid		
CC	(N2) that hybridizes under stringent conditions to N1; (3) an expression		
CC	cassette comprising N1 under the transcriptional regulation of a		
CC	transcriptional initiation region functional in an expression host, and a		
CC	transcriptional termination region; (4) a cell comprising an expression		
CC	cassette of (3) as part of an extrachromosomal element or integrated into		
CC	the genome of a host cell as a result of induction of the expression		
CC	cassette into the host cell, and the cellular progeny of the host cell;		
CC	(5) a method for producing a P1 comprising growing a cell of (4) where		
CC	the protein is expressed and isolating the protein free of other		
CC	proteins; (6) a purified polypeptide composition comprising at least 50		
CC	weight % of P1; and (7) a monoclonal antibody binding specifically to the		
CC	peptide of (6).		
XX			
SO	Sequence 273254 BP; 76423 A; 51054 C; 61965 G; 83812 T; 0 other;		
Alignment Scores:			
Pred. No.:	2,1e-96	Length:	273254
Score:	1435.50	Matches:	340
Percent Similarity:	51.43%	Conserves:	147
Best Local Similarity:	35.90%	Mismatches:	335
Query Match:	33.42%	Indels:	125
DB:	21	Gaps:	15

US-09-830-446-27 (1-841) x AAC81914 (1-273254)

QY	1	MelYelIeProLeuAtrPheLeuLeuIleSerLeuValProThirLeuSerMetSerAen	20
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QY	21	LeuLeuClYalAlaThrThrGluGluLeuSerAlaSerAenSerPheApoGlyThrThc	40
Db	97974	CTACAGTCACTACCTAACGAGAACTTTATACCTGATGATAGCTTATAGAAATATC	97915
QY	41	SeThrThrSerPheSerSerIyThrSerSerAlaThrApoGlyThrAnTyThrValPhe	60
Db	97914	GATTACAGAACGTTTACTCCAAAACCTTACGC-----ACAAATATTCCTCA	97865
QY	61	LyAaPserValValIleGluAenValProLyThrGlyGluThrGlnSerThrSerCyS	80
Db	97866	ACAGAGATGATCTCTTTTACGAG--CCTGGAAAAGCAGCTCCCTTATACAGTTGT	97810
QY	81	PhelyAaenApoAlaAlaIleGlyAaPLeuAaenPheLeuGlyGlyGlyPheSerPheThr	100
Db	97809	TTTAAAGCA-----ACCACGAGACATCTTACTTTGGGAAACGCTATAGCTTAAAG	97766
QY	101	PheSerAaenIleAaPAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAaen	120
Db	97755	TTTGGCTTTATAGATGCTGCACTATGACAGGTCGCT--GCATCTACACAGCAAT	97699
QY	121	LyThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLySerProAlaSerThr	140
Db	97698	AAGATCTTACTCTTCAGGGTTTCTTACTAGATGTTGATTCTCTCTGACCAACG	97639
QY	141	ValThrAaenGlyLeuGlyAlaIleAaenValLySgLyAaenLeuSerLeuAaenAaP	160
Db	97638	GTTACTACAGGTACGAGAACGCTTCTCAGCAGAGGGGTAAATTTAAATAATTCGT	97579
QY	161	LyValLeuIleGlnAaPhePheSerThrGlyAaPGLyGlyAlaIleAaenCyAlaGly	180
Db	97578	AAACTTATAGTCTGGAATTTTCTTACTGCAAGATGATGAGACTATCAAAGAGCTCT	97519
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Db	97518	TTTCCTTTAACTGGCACTTGAGATGCTTTTATTAACAACCTTCATCAACAAG	97459
QY	180	-----	180
Db	97458	GAGAGCAATTGCTACTACAGACAGCGCTCGCATAGCAATTAACAAGTTATGTAGA	97399
QY	180	-----	180
Db	97398	TTTCCTATCAATAGCGCTTACGTACAGAGCGCTATAGATGATGAAGCAGCTGATA	97339
QY	180	-----	180
Db	97338	CTATCGAACAAATTTCTATTTTGAAGGGAATGACGCGAAACTACTGCGCGTGGC	97279
QY	181	-----SerLeuLyIleAlaAaenAaenLySerLeu	190
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QY	191	SePheIleGlyAaenSerSerThrAaPGLyGlyAlaIleHisThrLyAaenLeuThr	210
Db	97218	ATCTTCTTCAACGATGACGAAACAAAGCGGGGCGCACTCATCTTAAAAAGTACGC	97158
QY	211	LeuSerSerGlyGlyThrLeuPheGlnGlyAaenThrAlaProThrAlaAlaGlyLyS	230
Db	97158	CTTTCCTCTGAGGCTTTACAGGTTTCTACGAAATATATGTCTCAACACCACTCTAAG	97099
QY	231	GlyGlyAlaIleAlaIleAaPserGlyThrLeuSerIleSerGlyAaPserGlyAaP	250
Db	97098	GGGGGTCTACTACGATCGATGCTCAGAGAGACTCAGTCTTTCGACAGACAGCAAC	97039
QY	251	IleIlePheGlnGlyAaenThrIle-----GlyAlaThrGlyThrAlaSerHisSer	267
Db	97038	ATTACCTTTTAAAGAAATACCTTACAAACCGAAAGTACGATCTCTTAAAGTAT	96979

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus_p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 4263 Seconds
(without alignments)
4794.761 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4295
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Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 22781392 seqs, 12152238056 residues

Total number of hits satisfying chosen parameters: 45562784

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Command line parameters:
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-DB=EST -QPMT=fastap -SUFFIX=2n.rst -MINMATCH=0.1 -LOGFC=0 -LOGPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blousum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pco -NORM=ext -HEAFSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US0830446.0CCN.1.1.3132.0runat.29012004.102102.19215 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -MARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :
EST:
1: em_estba:*
2: em_esthum:*
3: em_estin:*
4: em_estnu:*
5: em_estov:*
6: em_estpl:*
7: em_estro:*
8: em_hic:*
9: gb_est1:*
10: gb_est2:*
11: gb_hic:*
12: gb_est3:*
13: gb_est4:*
14: gb_est5:*
15: em_estfun:*
16: em_estom:*
17: em_gss_hum:*
18: em_gss_inu:*
19: em_gss_pln:*
20: em_gss_vit:*
21: em_gss_fun:*
22: em_gss_man:*
23: em_gss_mus:*
24: em_gss_pro:*
25: em_gss_rtd:*
26: em_gss_phg:*
27: em_gss_vrl:*
28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	157	3.7	915	29	CNS06GB1
2	155	3.6	624	12	BM276405
3	155	3.6	979	29	CNS06EDM
4	151	3.5	1094	29	CNS076CM
5	151	3.5	2293	11	AK032791
6	150.5	3.5	1022	9	AL543791
7	150.5	3.5	1792	11	AY103948
8	144	3.4	1164	13	BX405896
9	142	3.3	977	29	CNS0678C
10	142	3.3	1159	29	CNS076BD
11	141.5	3.3	1001	13	BQ963411
12	140.5	3.3	634	10	BE583883
13	140	3.3	779	14	CA318878
14	137.5	3.2	788	12	B3368874
15	135.5	3.2	698	14	CD284689
16	135	3.1	738	14	CA357513
17	135	3.1	739	28	AY079536
18	135	3.1	1150	29	CNS0792S
19	134.5	3.1	719	14	CA855416
20	133.5	3.1	849	28	AZ546009
21	133	3.1	755	14	CA486671
22	133	3.1	761	14	CA484808
23	132.5	3.1	739	28	AY079536
24	132	3.1	882	13	BQ723746
25	132	3.1	898	29	CNS04ALV
26	130.5	3.0	644	13	B0838510
27	130	3.0	731	14	CA485466
28	130	3.0	740	14	CA485375
29	130	3.0	833	12	B329437
30	129.5	3.0	905	29	CNS06LFI
31	129.5	3.0	965	29	CNS07DO3
32	129	3.0	672	14	CD047378
33	128.5	3.0	926	29	CNS06FRK
34	128.5	3.0	1200	14	CD497556
35	128	3.0	938	29	CNS07CG2
36	127.5	3.0	804	13	BUE02542
37	127.5	3.0	816	28	AZ535744
38	127.5	3.0	863	14	CB588445
39	127.5	3.0	2391	28	BH771003
40	127	3.0	695	12	B3388152
41	127	3.0	807	12	B412244
42	127	3.0	877	28	AZ531291
43	126.5	2.9	832	12	BM170146
44	126.5	2.9	1123	12	BM554825
45	126.5	2.9	2589	11	AK047537

ALIGNMENTS

RESULT 1
CNS06GB1 915 bp. DNA linear GSS 30-NOV-2001
LOCUS T3 end of clone AS0A003C01 of library AS0A from strain CLIB 533
DEFINITION of Saccharomyces bayanus, genomic survey sequence.
ACCESSION AL397475
VERSION AL397475.1 GI:12150179
KEYWORDS
SOURCE GSS.
ORGANISM Saccharomyces bayanus
Saccharomyces bayanus
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
REFERENCE 1 (bases 1 to 915)


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RESULT 2
BM276405/c
LOCUS      BM276405      624 bp      mRNA      linear      EST 20-DEC-2001
DEFINITION P530aa2a2f11.y1 Plasmodium falciparum 3D7 gametocyte cDNA library
            Plasmodium falciparum 3D7 CDNA 5' similar to SW:CIGB_DICD1_Q94481
            CIGB PROTEIN ;, mRNA sequence.
ACCESSION  BM276405
VERSION     BM276405
KEYWORDS    Plasmodium falciparum 3D7
SOURCE      Plasmodium falciparum 3D7
            Eukaryota; Alveolata; Apicomplexa; Haemosporida; Plasmodium.
REFERENCE   1 (bases 1 to 624)
AUTHORS     Tang,K., Cole,R., Chakrabarti,D., Haywood,R., Clifton,S., Page,D.,
            Matra,M., Hillier,L., Martin,J., Wylie,T., Danne,M., Theising,B.,
            Bowers,Y., Gibbons,M., Ritter,E., Bennett,J., Jenne,E., Ronko,I.,
            Tsagarisshvili,R., Belagorod,L., Franklin,C., Carr,L., Grow,A.,
            Maguire,L., Ritchey,J., Madhavi,J., Kennedy,S., Levinso,D.,
            Wareton,R., Wilson,R. and Sibley,D.
TITLE       Washu Plasmodium E8T Project
JOURNAL     Unpublished
COMMENT     Contact: L. David Sibley
            Washu Plasmodium E8T Project
            Washington University School of Medicine
            444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
            Tel: 314 286 1800
            Fax: 314 286 1810
            Email: est@watson.wustl.edu
            Library was constructed by R. Haywood. DNA sequencing by:
            Washington University Genome Sequencing Center For information on
            obtaining a clone please contact: L. David Sibley
            (sibley@borcim.wustl.edu), Washington University
            Seq primer: -400P from Gibbo
            High quality sequence stop: 430.
            Location/Qualifiers
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                /mol_type="mRNA"
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                /dev_stage="gametocyte (stage III-V)"
                /lab_host="DH10B (Genesig, Invitrogen, Inc.)"
                /clone_id="Plasmodium falciparum 3D7 gametocyte cDNA
                library"
                /note="Vector: pBluescript SK plus; Site_1: EcoRI; Site_2:
                XhoI; The library was constructed by R Haywood. cDNAs were
                synthesized from gametocyte poly(A)+ RNA by oligo d(T)
                priming, size-selected and directionally cloned into the
                EcoRI (5' end) to XhoI (3' end) sites of the Uni-ZAP XR
                lambda vector (Stratagene). The primary library was mass
                excised as phagemid using the ExAssist helper phage
                (Stratagene). Clones were mass excised using the ExAssist
                helper phage (Stratagene), the phagemids were precipitated
                with PEG 8000 and extracted with phenol/chloroform.
                Phagemid DNA was electroporated into DH10B cells. Clone
                Availability: David Sibley, Washington University."
BASE COUNT      261 a      61 c      158 g      144 t
ORIGIN
Alignment Scores:
Pred. No.:      1,27e-05      Length:      624
Score:          155.00      Matches:      60
Percent Similarity: 45.65%      Conservative: 45
Best Local Similarity: 26.09%      Mismatch: 97
Query Match:      3,61%      Indels:      28
DB:              12      Gaps:      8
US-09-830-446-27 (1-841) x BM276405 (1-624)
Oy      17 SerhetSerAenLeuLeuGlyAlaAlaIaThrGluGluLeuSerAlaSerAenSerPhe 36
        ||| ||| ::::| ::| ::| ::| ::| ::| ::| ::| ::| ::| ::|
Db      623 AGCTCTTAGGATACCTTCTCTACTAGTCTTCTTCGATATACCTCTTACGACTTCTT 564
Oy      37 AepglyThrThrSerThrThrSerPheSerSerlyThrSerSerAlaThrAspGlyThr 56

```

[illegible]

MEDLINE 20584716
 PUBMED 1152881
 REFERENCE 3 (bases 1 to 979)
 AUTHORS Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (07-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)
 COMMENT This GSS is part of a random genomic sequencing program of thirteen yeast species: *Saccharomyces bayanus* var. *uvarum*, *Saccharomyces exiguus*, *Saccharomyces servazzii*, *Zygosaccharomyces rouxii*, *Saccharomyces kluyveri*, *Kluyveromyces thermotolerans*, *Kluyveromyces lactis* var. *lactis*, *Kluyveromyces marxianus* var. *marxianus*, *Pichia angusta*, *Debaryomyces hansenii* var. *hansenii*, *Pichia sorbicola*, *Candida tropicalis* and *Yarrowia lipolytica*. Genomic inserts of 3 to 5 kb were prepared and both extremities were sequenced. See keywords for description of this sequence and for the sequence of the other extremity of this insert.

FEATURES
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 /strain="CBS 379"
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 /clone_1lb="AV0AA"
 /note="end : 77"
 Location/Qualifiers
 BASE COUNT 226 a 205 c 217 g 331 t
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 Alignment Scores:
 Pred. No.: 2,536-05 Length: 979
 Score: 155.00 Matches: 83
 Percent Similarity: 37.87% Conservative: 45
 Best Local Similarity: 24.56% Mismatches: 138
 Query Match: 3.61% Indels: 72
 DB: 29 Gaps: 13
 US-09-830-446-27 (1-841) x CNS06PDM (1-979)

DB 504 AACGCTTTA.....ACAAAC 487
 QY 199 ThraGlyGlyAlaIleHisThrLysAsnLeuThrLysSerGlyGlyThrLeu 218
 DB 486 ACTACAGGAAGCTGGTCAACATGATGTGTAACTTTAACTGAACATGATATAGT 427
 QY 219 PheGlnGlyAsnThrAlaProThrAlaIleGlyGlyGlyAlaIleAlaIleAsp 238
 DB 426 GCTCAATTACACATACAGGAACCTGGTCAACTGATGTAAATGTTCTCAAACTCAACC 367
 QY 239 SerGlyThrLysSerLysSerGlyAspSerGlyAspIleIlePheGlnGlyAsnThrIle 258
 DB 366 GATGGTATGGTTCTTCAACACACATACAGGAACCTGGTCAACCGATGTATGGTTCT 307
 QY 259 GlyAlaThr-----GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLys 276
 DB 306 CAAGTACACATGATGTATAGTGTCTTTAACTGCAACTGAT--GGTACAGTGTCTCA 250
 QY 277 IleThr-----AlaLeuArgAlaIleGlnGlyHisThrIleTyrPheTyr 291
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 QY 292 AspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsnLysSerPro 311
 DB 198 ---CAACTACACATACAGGAACCTGATCAAAATCCATGCAACAGATGTATACGGTTCC 142
 QY 312 AspThrGlyAspAsnLysGlyThrGlyThrIleValPheSerGlyGlu----- 328
 DB 141 CAACACACAGATGATGTATAGTATGATACATACACAACTAATGATGTATGATGATG 82
 QY 329 -----LysLeuThrGlnAlaGlnAlaLysAspGlyLysAsnArgThrSer 343
 DB 81 ATGGATCATCATCAATGATGATCTATAGATGAGCAAACTACAGAAACAAGC 28

RESULT 4
 CNS076CM/c
 LOCUS
 DEFINITION T3 end of clone BBOA002P11 of library BBOA from strain CBS 4732
 ACCESSION AL431228
 VERSION AL431228.1 GI:12214640
 KEYWORDS GSS.
 ORGANISM *Pichia angusta*
 SOURCE *Pichia angusta*
 ORGANISM *Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Pichia.*
 REFERENCE Soucier,J.L., Aigle,M., Artiguenave,F., Blandin,G., de-Montigny,J., Dujon,B., Bon,E., Brothier,P., Casaregola,S., Walpertuy,A., Neuvéglise,C., Ozier-Kalogeropoulos,O., Potier,S., Saurin,M., Takala,F., Toffano-Nioche,C., Wesolowski-Louvel,M., Winkler,P. and Weissenbach,J.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 1. A set of yeast species for molecular evolution studies
 JOURNAL FEBS Lett. 487 (1), 3-12 (2000)
 MEDLINE 20584711
 PUBMED 1152876
 REFERENCE Blandin,G., Llorente,B., Walpertuy,A., Winkler,P., Artiguenave,F. and Dujon,B.
 TITLE Genomic exploration of the hemiascomycetous yeasts: 13. *Pichia angusta*
 JOURNAL FEBS Lett. 487 (1), 76-81 (2000)
 MEDLINE 20584723
 PUBMED 1152888
 REFERENCE Genoscope.
 TITLE Direct Submission
 JOURNAL Submitted (08-SEP-2000) Genoscope - Centre National de Sequencage, 2 rue Gaston Cremieux, CP 5706, 91057 EVRY cedex, FRANCE. (E-mail : seqref@genoscope.cns.fr - Web : www.genoscope.cns.fr)

QY 214 GYGLVGLVThrluPhehnglnlYanThralaProThralaAlaGlyLysGlyAla 233
 DB 1330 GGTGGTAACTG-----GGCACTAGCGCTGGCTTGGATGAGACTGGGACACAGC 1380
 QY 234 TleAlaAlaAlaAspSerGlyThrluSerlleserGlyAspSerGlyAspIleIlePhe 253
 DB 1381 ACCAGCTTGGT---GCAGAGCTGGGACCTAGAGAGAGGCTTGGTGGTAACTG----- 1431
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 DB 1432 ---GGCAACCAATACCTGTTGGTGGCACA-----CTTGGCACT 1467
 QY 274 SerAlaIleIleThrl---AlaIleuArgAlaAlaGlnGlyHisThrlIleThrlPheThrlAsp 292
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 DB 1627 AATGAGCCAGCTTCTATTTGTTGCTTAACTGATGAGCAACAGCACTGGTGGCTTCTG 1686
 QY 372 PalaAsnSerLysLeuIleMetAspLeuGlyThrlSerIleValAlaAsnThrlGlySerIle 392
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 DB 1837 GAGGTGGCTTGGAGAGCAACAGCACTG-----GAGGTGGCTT 1875
 QY 447 TTYrAspGlyIleLeuGlnLeuAspAlaGlyLysAsp 459
 DB 1876 GGAGAGCAACAGCACTGAGGTG---GCTTGGAGAGC 1909
 RESULT 6
 AL543791 1022 bp mRNA linear EST 31-MAY-2003
 LOCUS AL543791 Homo sapiens PLACENTA COT 25-NORMALIZED Homo sapiens cDNA
 DEFINITION clone CS0D1005YD03 5-PRIME, mRNA sequence.
 ACCESSION AL543791
 VERSION AL543791
 KEYWORDS EST.31265637
 SOURCE Homo sapiens (human)
 ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
 REFERENCE 1 (bases 1 to 1022)
 AUTHORS Li, W.B., Gruber, C., Jessup, J. and Polayes, D.
 TITLE Pull-length cDNA libraries and normalization
 JOURNAL Unpublished
 COMMENT On Feb 15, 2001 this sequence version replaced gi:12876270.
 Contact: Genoscope
 Genoscope - Centre National de Sequencage
 BP 191 91006 EVRY cedex - France

Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
 Library was constructed by Life Technologies, a division of
 Invitrogen. This sequence belongs to sequence cluster 10829.f For
 more information about this cluster, see
 http://www.genoscope.cns.fr/
 cgi-bin/cluster.cgi?seq=CS0D1005CB020P1c1cluster=10829.f. Contact :
 Feng Liang Email : fliang@life.techn.com URL :
 http://fulllength.invitrogen.com/ invitrogen Corporation 1600
 Paraday Avenue Genoscope sequence ID : CS0D1005B02QP1.
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 BASE COUNT 195 a 282 c 277 g 265 t 3 others
 ORIGIN
 Alignment Scores:
 Pred. No.: 8.02e-05 Length: 1022
 Score: 150.50 Matches: 86
 Percent Similarity: 40.43% Conservative: 45
 Best Local Similarity: 26.54% Mismatches: 104
 Query Match: 3.50% Indels: 89
 DB: 9 Gaps: 15
 US-09-830-446-27 (1-841) x AL543791 (1-1022)
 QY 17 SerMetSerAnlleuLeuGlyAlaAlaThrlGlnGlyLeuSerAlaSerAnSerPhe 36
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 QY 37 AspGlyThrlThrlSerThrlThrlSer----- 44
 DB 219 GGAGGCACTCAGCACCAAGCTGGCTTAACTGATGAGTACTCAGCACTGACCACTTT 278
 QY 45 -----PheSerSerLysThrlSerSerAlaThrlAspGly 55
 DB 279 GGCAGTGCACCCACACAGACAGCACTTCACTAGTGGCTTGGACCAAGCACT---GGC 335
 QY 56 ThrAsnTy-ValPheLysAspSerValIleGluAnlleuValProLysThr----- 72
 DB 336 TTGGAGGCACTCAGCACAGTGTCTTTGGTGGTCTCCAGCTCCAGCTGAGTGGTAC 395
 QY 73 ---GlyLysThrlGlnSerThrlSer---CysPheLysAsnAspAlaAlaGlyAspLeu 90
 DB 396 TTGGTGTATCACTCAGTACAGTATCTGCTTC----- 428
 QY 91 AsnPheLeuGlyGlyGlyPheSerPheThrlPheSerAsnIleAspAlaThrlThrlAser 110
 DB 429 -----GGTGGCTCTCCGACACAGCACTGGCTTGGAGGCACTTACAGC 476
 QY 111 GlyAlaAlaIleGly-----SerGlnAlaAlaAsnLysThrlValThrlLeuSerGly 127
 DB 477 AGTGTCTCTTGGTGGCTTCCAGCACAGTGGCCAAATTTGGTGGTACACTAAGT--- 533
 QY 128 PheSerAlaLeuSerPheLeuLysSerProAlaSerThrlValThrlAnGlyLeuGlyAla 147
 DB 534 ---ACAGATCTGCTTATAGCTCTCCAGACAGTGGCTGGCTTGGT---GGTGT 587
 QY 148 IleAsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAn 167
 DB 588 CTCACACACAGTCCAGCTTGGC-----AGTGTCTC-----AAC 623
 QY 168 PheSerThrlGlyAspGlyAlaIleAnCyAlaGly-SerLeuLysIleAlaAsnAs 187
 DB 624 ACCAGTACTGGTTTGGTGGTGTATGACACACAGTGTGACTTGGCGGTACACTAAGC 683

QY 187 nlyseSerLeuSerPheIleGly-----As 195
 DB 684 ACACAGTGTCTGCTTGTGCTGCTCCGACACAGTGTGAGCTTGGCAGTGTGACCTCA 743
 QY 195 nSerSerSerThrArgGlyGlyAlaIleHisThrIys-----AsnLeuThrLeuSe 212
 DB 744 CACCAATGCTGTATATGCTGTGCTGTGACCAACACTGACTTGTGTGTACACTTAG 803
 QY 212 rSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGlyLysGly 232
 DB 804 CACC-----ACGCTGCTTTTGTGGCTCTCCACGACGAGTGTGCTTGTGGG 854
 QY 232 yAlaIle-----AlaIleAlaAspSerGlyThrLeuSerIleSerGly 246
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 QY 266 lAsSerAlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaIleGlnGlyH 286
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 QY 286 lThrIle 288
 DB 1008 ACTTAGTA 1015

RESULT 7
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 ACCESSION AY103948
 VERSION AY103948.1 GI:21207026
 KEYWORDS HTC.
 SOURCE Zea mays
 ORGANISM Zea mays
 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
 Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACAD
 clade; Panicoidae; Andropogoneae; Zea.
 REFERENCE 1 (bases 1 to 1792)
 Hainey,C.F., Dolan,M., Miao,G.H., Vogel,J.M., Whitesitt,M.S.,
 Arthur,L.M., Hanafey,M., Morgante,M. and Tingey,S.V.
 Maize Mapping Project/Dupont Consensus Sequences for Design of
 Overgo Probes
 Unpublished (2002)
 2 (bases 1 to 1792)
 Coe,E.H.
 JOURNAL Direct Submission
 REFERENCE Submitted (25-APR-2002) Maize Mapping Project, University of
 TITLE Missouri, Columbia, MO 65211, USA
 JOURNAL If you are interested in getting corresponding physical clones,
 COMMENT these are publicly available from ZmDB and may be found by BLAST
 searching at MSU, maizegap.org; ZmDB, www.zmdb.iastate.edu; TIGR,
 www.tigr.org; or NCBI, www.ncbi.nlm.nih.gov. When the source of the
 maize cDNA sequences is either Virginia Mahoe, Stanford or Pat
 Schnable, Iowa State, then clones may be requested from ZmDB:
 www.zmdb.iastate.edu.
 FEATURES
 SOURCE location/Qualifiers
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 /note="This sequence is part of a project of EST
 assemblies resulting from the application of public
 configs to seed Dupont configs; this resource was
 assembled by Dupont as part of a collaboration for the
 overgo addressing of Bacc in conjunction with the Maize
 Mapping Project"

BASE COUNT 467 a 506 c 482 g 337 t
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 Alignment Scores:
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 Best Local Similarity: 23.32% Mismatches: 157
 Query Match: 3.50% Indels: 91
 DB: 11 Gaps: 14
 US-09-830-446-27 (1-841) x AY103948 (1-1792)
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 DB 1414 TGCTGTCTCTCCTGCTTCCGCCT-----TTGTGCGGACGGCTG 1376
 QY 27 ThrGluLeuSerAlaSerAsnSerPheAspGlyThrThrSerThrSerPheSer 46
 DB 1375 TTCTTAGTGAAGCGGCTGTGCTCGCTCCAGCGCGGACATCAGTGGCGGACATCT 1316
 QY 47 SerLysThrSerSerAlaThrAspGlyThrAsnThrValPheLysAspSerValIle 66
 DB 1315 GCTTTG----- 1310
 QY 67 GluAsnValProLysThrGlyGluThrGlnSerThrSerCysPheLysAsnAlaIle 86
 DB 1309 -----GTCCCGGGTGTGATCAGCG-----GCCGCA 1283
 QY 87 AlaGlyAspLeuAsnPheLeuGlyGlyPheSerPheThrPheSerAsnIleAspAla 106
 DB 1282 GCATCTGATTTGATTGATTCAGGTGCTGATCAGCGGACGACAGGCTGCGCATCTGATTG 1223
 QY 107 ThrThrLaseGlyAlaIleGlySerGluAlaIleAsnLysThrValThrLeuSer 126
 DB 1222 GTTTCAGCGCTGAGCAGACACATCAGACAGCATTTGACACTGCTTGTGCTCG 1163
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 QY 147 AlaIleAsnValLysGlyAsnLeuSerLeuLeuAspAsnLysValIleLeuGlnAsp 166
 DB 1111 GCA-----GCACACGATCGACGACAGCATTCAGCACTGATTGCTCGGCG 1064
 QY 167 AsnPheSerThrGlyAspGlyAlaIleAsnCysAlaGlySerLeuLysIleAlaAsn 186
 DB 1063 ACTGAGACAGACAGACAGATTCAGCACTGATTTGTGTACGGCGCTGACGACGACGA 1004
 QY 187 AsnLysSerLeuSerPheIle---GlyAsnSerSerThrArgGlyGlyAlaIleHis 205
 DB 1003 GGCTCAGCACTGATTGTTGTGTACGACATCGACAGACAGACAGACAGGCTG----- 950
 QY 206 ThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
 DB 949 -----GCATCTGT-----TTGTTTTCAGCGCTGCGGCGAGA 917
 QY 226 ThrAlaIleGly-----LysGlyGlyAlaIleAlaIleAlaAsp 238
 DB 916 ACACAGACAGGCTTGGCATCTGTTGTTCAGGCGCTGGGCGAACAACGACGACGGC 857
 QY 239 SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGlnGlyAsnThrIle 258
 DB 856 TCGGCACTGATTGCTCAGGACGACGAGGGA-----GGAAACGACGA 812
 QY 259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
 DB 811 GGCTCGGACAGACAGCGGCTGAAGTTGCTGAGTGTCTTACTGAGCTGAGCGACCA 752
 QY 279 AlaLeuArgAlaIleGlnGlyHisThrIleThrPheThrAspProIleThrValThrGly 298
 DB 751 GCT---TCAGGCTCATGTGCTTGGCATCTTCTTCTTCCTCCGATTTGGCAAGAGA 695

[illegible]

Oy		89	nApLeuAnBpheUeuGlygyl---GlyPheSerPheThrPheSerAenile---AspAla	106
Db		179	GAGTCTCTACTACTGGCGGTGCTGGTAGTCCTCTACTACTGGTGCTGCAGATCC	238
Oy		107	ThcThrAlaserGlyAlaAlaIleGlySerglu-----AlaAlaenUsthrValThr	124
Db		239	TCTACTACTGGCGGTGCTGGTAGTCCTCTACTACTGGCGGTGCAGATCCTCTACT	298
Oy		125	LeuSerGlyPheSerAlaleuSerPheUeuLySerProLa---SerThrValThrAsn	143
Db		299	ACTGGCGGTGCTGGTAGTCCTCTACTACTGGCGGTGCTGGCGAGTCTCTACTACTGGC	358
Oy		144	GlyLeuGlyAlaIleAleuValYsglyYasnLeuSerLeuUspAenAplyeValleu	163
Db		359	GGTGCTGGTAGTCCTCTACTACTGGCGGTGCTGGC-----	394
Oy		164	IleGlnAapAanBpheserThrglyAmpGlyGlyAlaIleAanCyalaGlyserLeuys	183
Db		395	-----GAGTCTCTACTACTGGCGGTGCTGGTAGTCCTCTACTACTGGCGGT-----	442
Oy		184	IleAlaAanBanUlysSerLeuSerPheIleGlyYasnSerSerThrAargGlyYAla	203
Db		443	---GCTGGCGAGTCTCTACTACTGGGGGGTGGCTGGTAGTCCTCTACTACTGGTGCT	499
Oy		204	IleHisThrlyAanUleuthrLeuSerSerGlyGlyGlyUthrLeuPheGlnGlyAsnthr	223
Db		500	GCGAGTCACTTCTGCTGCTTCCACACTAGTGtGT-----GCTGGCGAG	544
Oy		224	AlaProThralaAlaglyGlyGlyYAlaIleAlaIlealAapSerGlyYthLeuSer	243
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Oy		264	ValSerHiasSerAlaIleAapLeuGly-----ThrSerAlaYsnIleThr	278
Db		653	TGGTCTTGTGCTGCTTCCACACTAGTGGTGGTGGTGGTAGTCGTCTGCTGCTTCCACT	712
Oy		279	AlaLeuAargAlaAlagInGlyHisIleThrlIetyrPheYrAapProIleThlValThnGly	298
Db		713	ACTGGTGGTGGTGGTGGTCTCTACTACTGGTGGTGGTGGCGAGTCTCTACTACTGGC	772
Oy		299	SerThrSerValAlaAapAlaUeuAmUlaanserProAapThrglyAaspAunUysglu	318
Db		773	GGTGTGGCGAGTCTCTGCTACCAGA---CAGTCTACTAGTGCACAACACTCCAACACC	829
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Db		830	AACACAGGCGGTGGAG---ACTGGTTCTAAACACTGCCTCTACTACTAGCGGTGACGGT	886
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LOCUS		T7 end of clone BBOA001064 of library BBOA from strain CBS 4732		
DEFINITION		of Pichia angusta, genomic survey sequence.		
ACCESSION		AL431075		
VERSION		AL431075.1 GI:12214487		
KEYWORDS		GSS.		
SOURCE		Pichia angusta		
ORGANISM		Pichia angusta		
REFERENCE		Bukharova, Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;		
AUTHORS		Saccharomycetales; Saccharomycetaceae; Pichia.		
		1 (bases 1 to 1159)		
		Souciat,J.L., Aigle,M., Artigueave,F., Blandin,G.,		
		Boiclot,P.,Kuhara,M., Bon,E., Broctier,P., Casaregola,S.,		
		de-Montigny,J., Dujon,B., Durenne,P., Lepingle,A., Llorente,B.,		

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNLN)
 DNA Sequencing by: Agencourt Bioscience Corporation
 Clone distribution: MGC clone distribution information can be
 found through the I.M.A.G.E. Consortium/LNLN at:
<http://image.lnl.gov>
 Plate: L14M14077 row: K column: 24
 High quality sequence start: 22
 High quality sequence stop: 703
 Location/Qualifiers

1.1001

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 NotI; cloned unidirectionally. Primer: Oligo dT. Average
 insert size 1.7 kb. Constructed by Reagen, Invitrogen
 Corp. Note: this is a N1H MGC library."

BASE COUNT 196 a 255 c 276 g 272 t 2 others

ORIGIN

Alignment Scores:

Pred. No.:	0.000685	Length:	1001
Score:	141.50	Matches:	79
Percent Similarity:	36.57%	Conservative:	34
Best Local Similarity:	25.57%	Mismatches:	105
Query Match:	3.29%	Indels:	91
DB:	13	Gaps:	14

US-09-830-446-27 (1-841) x BQ963411 (1-1001)

QY 30 LeuSerAlaSerAenSerPheAapGlyThrThrSerThrThrSerPheSerSerlyThr 49
 DB 24 CTCACCAACAACACAGCTTGGCGAGTGACACACTACACAGCAGCTGTTCAGTGTGCA 83
 QY 50 SerSerAlaThrAapGlyThrAenTyValPheValAapSerValValIleGluAanVal 69
 DB 84 GTTACTACACCACTGGC----- 101
 QY 70 ProlyThrGlyGluThrGlnSerThrSer---GlyPheValAanAapAlaAlaIleGly 88
 DB 102 -----TTTGAAGGCACTTACACACAGCTGTCTGCTTT-----GCT 137
 QY 89 AspLeuAenPheLeuGlyGlyGlyPheSerPheThrPheSerAanIleAapAlaThrThr 108
 DB 138 AGTCTCCCTACTCTGGCGCTGCTTGGAGGACACACTTAACT- 179
 QY 109 AlaSerGlyAlaAlaIleGlySerGluAlaAlaAanlyThrValThrLeuSerGlyPhe 128
 DB 179 ----- 179
 QY 129 SerAlaLeuSerPheLeuLySerProAlaSerThrValThrAanGlyLeuGlyAlaIle 148
 DB 180 ACCAGATCTCTTGTGGTGTCTCTACACAC-----AATACGTGTTTGT- 227
 QY 149 AenVallyGlyAanLeuSerLeuLeuAapAanAaplyValIleIleGlnAapAanPhe 168
 DB 228 -----GGTACACTAGC-----ACCAAGTTTCTCTGGCTCTCTCT 266
 QY 169 SerThrGlyAap-----GlyGlyAlaIleAanCyValAaGlySerLeuLyIleAlaAan 186
 DB 267 AGCACACAGCTCTGACTTGTGGTGACACTAACACACTAGTCACTTGTGGCTGCTCTCT 326
 QY 187 AenlySerLeuSerPheIleGly-----AenSerSerSerThrArgGlyGlyAlaIle 204
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 QY 205 HisThrlyAanLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAanThrAla 224
 DB 387 AGCACC-----AGCACTGGC-----TTTGGCAGTGCATCTC 416

QY 225 ProThrAlaAlaGlyLyGlyGlyAlaIleAlaIleAlaAapSerGlyThrLeuSerIle 244
 DB 417 AATAACAGTGCACACTTGTGGTGGTCAATGATACCAAGCTTATGATGATCAATAGC 476
 QY 245 SerGlyAapSerGlyAapIleIlePheGluGlyAanThrIleGlyAlaThrGlyThrVal 264
 DB 477 AGTCCACAGCTTGTGGTGGCTATC-----AACACAGTGGTGGCTTGGCAGTACA 527
 QY 265 SerHisSerAlaIleAapLeuGlyThrSerAlaLyIleThrAlaLeuAalAlaGln 284
 DB 528 CTCACACAGAGTGCACACTTGTGGAGTGACCTACACACAGTGCACACTTGTGGT- 584
 QY 285 GlyHisThrIleTyPheTyAapProIleThrValThrGlySerThrSerValAlaAap 304
 DB 585 -----GTACTCAATGACAGTGTGCTGCTTGTGGT 614
 QY 305 AlaLeuAanIleAenSerProAapThrGlyAapAanlyGlyTyThrGlyThrIleVal 324
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 QY 325 PheSerGlyGlyTyLeuThrGlyAla 333
 DB 666 TTGTGTGGTGCATGACCAATGAC 692

RESULT 12

BE583883

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

COMMENT

CONTACT: Gijzen M

AgriCulture and Agri-Food Canada

1391 Sandford Street, London, Ontario, Canada N5V 4T3

Tel: 519 457 1470

Fax: 519 457 3997

Email: gijzenm@agr.ca

Transcript obtained from mixed plant-pathogen interaction culture.

Location/Qualifiers

1.634

/organism="Glycine max/Phytophthora sojae mixed EST

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/mol_type="mRNA"

/strain="Phytophthora sojae race 2 strain P6497"

/cultivar="Glycine max cultivar Harosoy"

/db_xref="taxon:135715"

/tissue_type="Plant hypocotyle infected with Phytophthora

sojae"

/dev_stage="8 d old etiolated hypocotyle 48 h

post-inoculation with Phytophthora sojae zoospores"

/lab_host="E. coli strain XL04R"

/clone_1lb="PsojaeHA"

/note="Vector: pAK-CMV; Site 1: EcoRI; Site 2: XhoI; This

cDNA library was constructed from polyA+ enriched mRNA

from etiolated hypocotyle 48 h post-inoculation with

Phytophthora sojae zoospores. Complementary DNA was

synthesized from mRNA using an XhoI-poly(dT)

linker-primer. EcoRI adapters were ligated to the

blunt-ended cDNA fragments and the products were digested

with XhoI for directional cloning into lambda ZAP Express

vector. This lambda library was amplified once using E.

coli host strain XL1 Blue MRP. Inserts were then


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Db      24 AGTACCAACCTGCTTAGTGCACACCAACAGCTTGGACGACCAACT 83
Qy      51 SerAlaThrAspGlyThrAsnValPheIleAspSerValIleGluAsnValPro 70
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Qy      71 LysThrGlyGluThrGlnSerThrSer---CysPheIleAspAlaIleAlaGlyAsp 89
      123 GCGTTTGAAGGACACTTAGACAGAGTGTGCTTT-----GTTAGT 164
Qy      90 LeuAsnPheLeuGlyGlyIlePheSerPheThrPheSerAsnIleAspAlaThrThrAla 109
      165 TCTCCCTACTCTGGGCGCTTGGAGGACCACTTAGT----- 203
Qy      110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnValThrValThrLeuSerGlyPheSer 129
      204 -----ACG 206
Qy      130 AlaLeuSerPheLeuLeuSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsn 149
      207 AGTATCTCTTGTGGTGGCTCTCTAGACCC-----AATACTGTGTTTGT----- 251
Qy      150 ValIleGlyAsnLeuSerLeuLeuAspAsnAspIleValIleGluAsnAsnPheSer 169
      252 -----GTTACTACTAGC-----ACCAGTGTTCCTTGGGCTTCTTCTAGC 293
Qy      170 ThrGlyAsp-----GlyGlyAlaIleAsnValAsnGlySerLeuLeuIleAlaAsn 187
      294 ACCAGCTCTGACTTGTGGTGGACACTAGACCAAGTGTGCTTGGTGGCTTCTGTGT 353
Qy      188 LysSerLeuSerPheIleGly-----AsnSerSerThrAsnGlyGlyAlaIleAsn 205
      354 GCCAATGTGGCTTGTGGCGGTACTCAACAGACAGTCAAGCTTGGCGGTCCATCCAGC 413
Qy      206 ThrIleAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaPro 225
      414 ACC-----AGCACTGGC-----TTTGGCAGTGCATCAT 443
Qy      226 ThrAlaAlaGlyIleGlyAlaIleAlaIleAlaIleAspSerGlyThrLeuSerIleSer 245
      444 AACAGTGCACACTTGTGGTGGTGCATAGTACCAAGCTTAGTGTGACTCATAGCAGT 503
Qy      246 GlyAspSerGlyAspIleIlePheGlnGlyAsnThrIleGlyAlaIleThrGlyThrValSer 265
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Qy      266 HisSerAlaIleAspLeuGlyThrSerAlaIleValIleThrAlaLeuArgAlaIleGlnGly 285
      555 AACAGACAGTGCAGCTTGTGGTGGTGCATGCACAGACAGTCCAGCTTGGTGGT----- 608
Qy      286 HisThrIleIleThrPheThrAspProIleThrValThrGlySerThrSerValAlaAspAla 305
      609 -----GTACTCAATGCGACAGTGTGGCTTGGTGGTGGC 641
Qy      306 LeuAsnIleAsnSer-ProAspThrGlyAspAsnIleGlyThrGlyThrIleValPhe 325
      642 TTGAACACCAATGCGACCTTGTGGTGGT-----GTACTCAATGCGAGTGTGGCTT 692
Qy      325 eSerGlyGlyIleLeuThrGluAla 333
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RESULT 14
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DEFINITION dictyostelium discoidium cDNA library, CP Dictyostelium
ACCESSION  BJ368874.1 GI:19278257
VERSION     BJ368874.1
KEYWORDS    EST.
SOURCE      Dictyostelium discoidium
ORGANISM    Dictyostelium discoidium
            Eukaryota; Eukaryota; Dictyostelid; Dictyostelium.

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REFERENCE 1 (bases 1 to 788)
AUTHORS   Urushihara,H., Tanaka,Y., Kohara,Y. and Shin-I,T.
TITLE      Full length cDNA of Dictyostelium discoidium at the culmination
            stage
JOURNAL    Unpublished
COMMENT    Contact: Tadasu Shin-I
            Center for Genetic Resource Information
            National Institute of Genetics
            111 Yata, Mishima, Shizuoka 411-8540, Japan
            Tel: 81-559-81-6856
            Fax: 81-559-81-6855
            Email: tahin@genes.nig.ac.jp.
            Location/Qualifiers
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US-09-830-446-27 (1-841) x BJ368874 (1-788)
Qy      64 ValIleIleGluAsnValProIleThrGlyGluThrGlnSerThrSerCysPheIleAsn 83
      27 ATAATGTCAACAACATTATTGTTGGTACAGTTCATCACTCATCATATTATTGGTTCA 86
Qy      84 AspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyIlePheSerPheThr----- 100
      87 ACACCTTACAGCAGGTGATTA-----TTTGTGTGTGTGATTAACAACAACACCAACA 140
Qy      101 -----PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGly 115
      141 GCGGTGTGTGTATTATTTGAGGTGCTCAACACACAGACAGCGCGGTATTATT 200
Qy      116 SerGluAlaAlaAsnIleThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuIle 135
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Qy      136 SerProIleSerThrValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSer 155
      243 GGAGTGTCTTCAACA-----ACACCAAGCAGTGTGTGTGTATTATTGGAGTGTAGTAC 299
Qy      156 LeuLeuAspAsnAspIleValIleIleIleAsnPheSerThrGlyAspGlyGlyAla 175
      300 ACTACAGACACA-----GCAACAGGTGTGTGTGTGTTA 332
Qy      176 IleAsnValIleGlySerLeuLeuIleAlaAsnAsnIleSerLeuSerPheIleGlyAsn 195
      333 TTT-----GGTGTCTTCAACAACACTGCACACAGAACTACTGAGGATTATTGGAGT 386
Qy      196 SerSerSerThrAspG-----GlyGlyAlaIleHisThr 206
      387 AGTACACTTACAGCAGCATCAACAACAAGTGTGATTATTGGAGTGTCTTCAACAACCT 446
Qy      207 LysAsnLeuThrLeuSerSerGlyGlyIleThrLeuPheGlnGly-----AsnThrAla 224
      447 ACACCATCAATTAACAACAACAGAGAGA-----TTATTGGAGTGTCTTCAACAACCTGCA 500
Qy      225 Pro-----ThrAlaAlaGlyIleGlyIleGlyAlaIleAlaIleAspSerGlyThrLeu 242

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GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 / Search time 121 Seconds
(without alignments)
3067.795 Million cell updates/sec

Title: US-09-830-446-27

Perfect score: 4295
Sequence: 1 MKPLPFLILSVPTLSMSN.....FEWRGSSRSYNDAGSKIF 841

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Delop 6.0, Delext 7.0

Searched: 569978 seqs, 220691566 residues

Total number of hits satisfying chosen parameters: 1139956

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-DEV TIMEOUT=120 -WARM TIMEOUT=30 -THREDS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

- 1: Issued Patents_NA.*
- 2: /cgml2_6/ptodata/1/ina/5A.COMB.seq.*
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- 6: /cgml2_6/ptodata/1/ina/BACKFILE1.seq.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	4255	99.1	1230025	4	US-09-198-452A-1
2	1365	31.8	1230025	4	US-09-198-452A-1
3	939	21.9	3021	4	US-09-556-877-182
4	939	21.9	3021	4	US-09-620-412C-182
5	939	21.9	3021	4	US-09-558-419-182
6	936	21.8	2949	4	US-09-556-877-170
7	936	21.8	2949	4	US-09-620-412C-170
8	936	21.8	2949	4	US-09-558-419-170
9	711.5	16.6	2643	4	US-09-556-877-169
10	711.5	16.6	2643	4	US-09-620-412C-169
11	711.5	16.6	2643	4	US-09-558-419-169
12	696.5	16.2	2601	4	US-09-556-877-181

13	696.5	16.2	2601	4	US-09-620-412C-181	Sequence 181, App
14	696.5	16.2	2601	4	US-09-558-419-181	Sequence 181, App
15	527.5	12.3	2895	4	US-09-556-877-171	Sequence 171, App
16	527.5	12.3	2895	4	US-09-620-412C-171	Sequence 171, App
17	527.5	12.3	2895	4	US-09-558-419-171	Sequence 171, App
18	527.5	12.3	2934	4	US-09-556-877-183	Sequence 183, App
19	527.5	12.3	2934	4	US-09-620-412C-183	Sequence 183, App
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21	506	11.8	5265	4	US-09-556-877-174	Sequence 174, App
22	506	11.8	5265	4	US-09-620-412C-174	Sequence 174, App
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24	447.5	10.4	5331	4	US-09-556-877-173	Sequence 173, App
25	447.5	10.4	5331	4	US-09-620-412C-173	Sequence 173, App
26	447.5	10.4	5331	4	US-09-558-419-173	Sequence 173, App
27	433	10.1	4593	4	US-09-556-877-172	Sequence 172, App
28	433	10.1	4593	4	US-09-620-412C-172	Sequence 172, App
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31	430.5	10.0	2547	4	US-09-620-412C-184	Sequence 184, App
32	430.5	10.0	2547	4	US-09-558-419-184	Sequence 184, App
33	421	9.8	2847	4	US-09-556-877-186	Sequence 186, App
34	421	9.8	2847	4	US-09-620-412C-186	Sequence 186, App
35	421	9.8	2847	4	US-09-558-419-186	Sequence 186, App
36	341	7.9	2103	4	US-09-620-412C-344	Sequence 344, App
37	341	7.9	2103	4	US-09-558-419-344	Sequence 344, App
38	333	7.8	2076	4	US-09-620-412C-312	Sequence 312, App
39	333	7.8	2076	4	US-09-558-419-312	Sequence 312, App
40	290	6.8	2148	4	US-09-620-412C-328	Sequence 328, App
41	290	6.8	2148	4	US-09-558-419-328	Sequence 328, App
42	266	6.2	1965	4	US-09-620-412C-340	Sequence 340, App
43	266	6.2	1965	4	US-09-558-419-340	Sequence 340, App
44	266	6.2	2052	4	US-09-620-412C-356	Sequence 356, App
45	266	6.2	2052	4	US-09-558-419-356	Sequence 356, App

ALIGNMENTS

RESULT 1
US-09-198-452A-1
Sequence 1, Application US/09198452A
Patent No. 6539294
GENERAL INFORMATION:
APPLICANT: Griffiths, R.
TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prev
TITLE OF INVENTION: and treatment of infection
FILR REFERENCE: 9710-003-999
CURRENT APPLICATION NUMBER: US/09/198,452A
CURRENT FILING DATE: 1998-11-24
NUMBER OF SEQ ID NOS: 6849
SEQ ID NO 1
LENGTH: 1230025
TYPE: DNA
ORGANISM: Chlamydia pneumoniae
FEATURE:
NAME/KEY: misc feature
LOCATION: (1)..(15000)
OTHER INFORMATION: n=a or c or g or t
NAME/KEY: misc feature
LOCATION: (15001)..(30000)
OTHER INFORMATION: n=a or c or g or t
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Alignment Scores:

Pred. No.:	0	Length:	1230025
Score:	4255.00	Matches:	840
Percent Similarity:	99.76%	Conservative:	0
Best Local Similarity:	99.76%	Mismatches:	1
Query Match:	99.07%	Indels:	2
DB:	4	Gaps:	0

US-09-830-446-27 (1-841) x US-09-198-452A-1 (1-1230025)

QY 1 MetIyIleProleuArpPheleuIleSerleuValProthrleuSerMetSerAa 20
 DB 28950 ATGAAGATTCACCTCCGCTTTTATGATATCATTTAGTACTACGCTTTCTATGCAAT 29009
 QY 21 LeuIeuGIYAlAlaIthrThrgIuIeuSerAlSerAaSerPheAapGIYThr 40
 DB 29010 TTAATGAGAGCTGCTCTACCGAAGAGTTATCCGCTAGCAATGCTCATGAGACTCA 29069
 QY 41 SerThrThrSerPheSerleuThrSerSerAlaThrAapGIYThrAaThrValPhe 60
 DB 29070 TCACACACAGCTTTCTTCTGTAACACATCATCGCTACAGATGGACCAATTAATGTTTT 29129
 QY 61 LysAapSerValAlaIleGIuAaenValProlyeThrgIYIuThrgIuSerThrSerCys 80
 DB 29130 AAAGATTCGTGATGTTATAGAAATGTACCAAAACAGGGAACTCAGCTACTACTGT 29189
 QY 81 PheIyAaenAaPAlAlaIaIagIyAaPLeuAaenPheIeuGIYGIYIyPheSerPheThr 100
 DB 29190 TTTAAATAAGACCTGCTCAGCTGAGATCTTAATTTCTTAGAGGGGGAATTTCTTCACA 29249
 QY 101 PheSerAaenIleAaPAlaThrThraIaSerGIYAlaIaIleGIYSerGIUAlaIaAaen 120
 DB 29250 TTTAGCAATATCATATCAACACAGGCTTCGAGCTGCTAATGGAAAGTAAAGACGCTAAT 29309
 QY 121 LysThrValThrIeuSerGIYPheserAlaIeSerPheIeuIySerProIaIaSerThr 140
 DB 29310 AAGACGCTACGCTATACAGATTTTCGCACTTTCTTTCTTAATCCCAAGCAATACA 29369
 QY 141 ValThrAaenGIYleuGIYAlaIleAaenValIyGIYAaenIeuSerleuAaPaaAaP 160
 DB 29370 GTGACATTAAGGATGGAGCTATCATATTAAGGAAATTAAGCTAATGGATTAATGAT 29429
 QY 161 LysValIleuIleGIuAaenAaPheSerThrgIyAaGIYGIYAlaIleAaenCysAlaGIY 180
 DB 29430 AAGGATTAATATTCAGCAATATTCACACAGAGAGAGGCGACA-ATTAAATGTGACGAC 29488
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 DB 29489 TCTTGAAGATCGCAACATTAAGTCCCTTTCTTTATTTGAAATAGTTCTTCACACACT 29548
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DB 29549 GCGGAGCAATTCATACCAAAAACCTCACATATCTTGTGGGGAAACTTAATTCAG 29608
 QY 221 GIYAaenThrAlaProthraIaIaGIYIyGIYAlaIleAlaIleAaPaaSerGIY 240
 DB 29609 GGGAAATACGGCCCTACCGCTGTGTAAAGAGGTGCTATCCGATTTGACAGCTCTGGC 29668
 QY 241 ThrIeuSerIleSerGIYAaPaaSerGIYAaPaaIleIlePheGIUAlaIleGIYAla 260
 DB 29669 ACCCTATCATTTCTTGACACAGTGGCACAATATCTTTGAAGGCAATACGATAGAGCT 29728
 QY 261 ThrGIYThrValIserIleSerAlaIleAaPLeuGIYThrSerAlaIyIleThrAlaIe 280
 DB 29729 ACAGGAACCGTCTCATATGTCTATTTAGTAAGAACTAGGCTTAAGTAATCTGGCTTA 29788
 QY 281 ArgAlaAlaGIYAlaIleThrIleThrPheThrAaPProIleThrValThrGIYSerThr 300
 DB 29789 CTTGCTGCCAAGACATACGATATCTTTATGATCCATTAATCTTAACAGGATGACA 29848
 QY 301 SerValAlaAaPAlaIeAaenIleAaenSerProAaPThrGIYAaPaaenIyGIYThr 320
 DB 29849 TCGTTGCTGATGCTCTCAATTAATTAATACCTGATACGAGATTAACAAAGATTAAG 29908
 QY 321 GIYThrIleValPheSerGIYGIYIySerleuThrgIuAlaGIUAlaIyAaPGIYIyAaen 340
 DB 29909 GGAACCATATGCTCTTTCTGAGAGAAAGCTCACGGAGCGCAAGCTAAAGATGAGAAAC 29968
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 DB 29969 CGCACTTCAATATCTTCAAAATGCTGCTTTAAATAAGGACGTGATTTGAAATAAG 30028
 QY 360 YAaPValIleuSerAlaAaenGIYPheserGIuAaPaaenSerIyIeuIleAaen 380
 DB 30029 TGAATGCTTTTAAGTGCAAGGTTTCTCAGATGCAAACTCAATGATTAATGA 30088
 QY 380 PLeuGIYThrSerleuValAlaAaenThrgIuSerIleGIUleuThraenIeuGIYIleAa 400
 DB 30089 TTTAGGAGAGCTGCTGTTGTCAAACACCAAAAGTATCGATTACGAATTTGAAATAAT 30148
 QY 400 nIleAaPserIeAaAaenGIYIyIySerIleIyIeuSerAlaIleThrAlaGIUlyAa 420
 DB 30149 TATGACTCTTCAGAGACGGAAAAAGATTAACCTCAGTGTGCCACAGCTCAGAAACA 30208
 QY 420 PLeaArgIleAaPaaProValIleuAlaIleSerAaPaaIySerPheThrgIuAaenGI 440
 DB 30209 TATGCTATAGATTCGTCGTTGCTGATGCAATTCAGCATGAGATTTTATCAAAATAG 30268
 QY 440 YPheIeuAaenGIuAaPaaIleSerThraPaaGIYIleuGIuAaPaaIleGIYIyAaPaa 460
 DB 30269 CTTTTTGAATGAGACCAATTCATATGATGGATTTCTTGAGTTAGATGCTGGAAAGACAT 30328
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 QY 480 YLysTrpThrIleAaenIySerThraPaaPaaIyIyAaIaThrValIserTrpAlaIyGI 500
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 DB 30449 GAGTTTAAATCCCATGCTGAGACAGAGGCTCGTTAGTTCTTAATCTTTGGGGTTC 30508
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 Db 30929 TCATCGCATGAAAGACCGAGTCTTACCCGCCGCCGCCGCCGAGCTCTGACGATCATAC 30988
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 US-09-198-452A-1/c
 ; Sequence 1, Application US/09198452A
 ; Patent No. 6559294
 ; GENERAL INFORMATION:
 ; APPLICANT: Griffls, R.
 ; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragmente
 ; TITLE OF INVENTION: thereof and uses thereof, in particular for the diagnosis, prev
 ; TITLE OF INVENTION: and treatment of infection
 ; FILE REFERENCE: 9710-003-999
 ; CURRENT APPLICATION NUMBER: US/09/198-452A
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Alignment Scores:
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Percent Similarity: 51.04% Conservative: 161
Best Local Similarity: 34.27% Mismatches: 320
Query Match: 31.78% Indels: 151
DB: 4 Gaps: 22

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US-09-830-446-27 (1-841) x US-09-198-452A-1 (1-1230025)

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QY 1 MetIvEILPLeuAaRgPhelEuLeuLle---SerLeuValPProthrLeuSerMetSer 19
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DB 518200 ATGAATTCGCAATTTCCTGCTAGCTCTCTTCGCAATTCGATGTTTACTACTGTG 518141
    |||||

QY 20 AsnLeuLeuGlyAlaIaIaThrThrgIuLeuSerAlaSerAsnSerPheAspGlyThr 39
    ::::
DB 518140 TCCACGTGTTTCTGCTCACTGCTGAATAATATAGCCCTCGATGCTTTGACGGAAGT 518081
    |||||

QY 40 ThrSerThrThrSerPheSerSerlyThrSerSerAlaIaThrAspGlyThrAsnlyVal 59
    |||||
DB 518080 ACTAACACACGACCTATACCTCTTAA-----AATACGACCTAGTGAATGACTATACT 518027
    |||||

QY 60 PheIyAspSerValIaIaIleGluSerValProllyThrGlyIuThrGlnSerThrSer 79
    ::::
DB 518026 CTGACACGAGATATTAATCTGCAAAACCTT-----GGGATTCGGACGCTTTAAAGC 517976
    |||||

QY 80 -----CysPheIyAsnAspAlaIaIaGlyAspLeuAsnPheLeuGlyGlyPhe 97
    |||||
DB 517975 AAGGCTGTTTCTGACACTACGGAATCT-----TTAAGCTTTCGCGTAAGGGGTAC 517922
    |||||

QY 98 SerPheThrPheSerAsnIleAspAlaIaIaIleGlySerGlu 117
    |||||

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Db 517921 TCACCTTCTTTTAAAT---ATNAGTCTAGTGTGAGGCGCANA-CTT---TCTGTT 517869
Qy 118 AAlaAaenlyeThrValThreuserglYpHeserAlaLeuserPheLeuysSerPro 137
Db 517868 ACACCTGATTAATAAATCTGTCCTAACAGGATTTGAGTCTTACTTCTTACGGGCCCA 517809
Qy 138 AAlaserThrValThr----- 142
Db 517808 TCATCGGTAATGACAAACCCCTCAGAGAAAGGTGAGTAAATGTGAGGGGATCTTACA 517749
Qy 143 -----AenGly-Leu----- 145
Db 517748 TTTGATTAACAATGAACTATTATTTAACAAGATTACTGTGAGAGAAATGCGGACAT 517689
Qy 145 ----- 145
Db 517688 TTCTACCAAGATCTTTCTTTGAAAAACGACGGGATGATTTCTTTGAAAGGAATTA 517629
Qy 145 ----- 145
Db 517628 ATCGAGCGCAACAGGAAAAAGGTGGGCTATTGTGCTACTGTGATCTGATATTAC 517569
Qy 146 -----GlyAla11 148
Db 517568 AATATAAGGCTCTTACCTCTCTCGAACATATTGTCGAGAGCTGACGTGAGCTAT 517509
Qy 148 eAnVallysglyAenLeuserLeuAenAenAenlyeValLeuLeuLeuAenAenAen 168
Db 517508 AATATGCAAGAAATGTAACATTTACAGGAAATGCTCTCTGTTATTTTCTGAAATATG 517449
Qy 168 eSerThr-----GlyAenPglYglYAla11eAenCyAalaglySerLeuYleu1 185
Db 517448 TGTGACAGGACCGCAGGAAATGAGAGACTCTTCTGAGANTGCGAGTACCATATC 517389
Qy 185 aAenAenlyeSerLeuserPhe11eGlyAenSerSerThrAenGlyYglYAla11eH 205
Db 517388 TCGGATTCAGAGGTGTAATCTTCTCAGAGAAACCAACGTGATGCTAATGGCGGACCATTTA 517329
Qy 205 eThrlyAenLeuThreuserSer-----GlyYglYglYThreLeuPhe-GlnGlyA 222
Db 517328 TCTTAAGAGCTTACCTGCTTCCGGGGGGGGGGGGGGTATCTCTTTCTTAACATA 517269
Qy 222 eThrThrAlaProThrAlaAalaglyYglYglYAla11eAalAenSerGlyThrL 242
Db 517268 TATGCAAGGTACCACTGACAGTAATGTGAGGCACTTCTATCTGAGCGAGCGAGAT 517209
Qy 242 euser11eSerGlyAenSerGlyAenPhe11ePheGlnGlyAenThr11eGlyAlaThr- 261
Db 517208 GTAGTCTTTCACAGAGAGGAGGACATTACCTTCATGAGGATGCCATTGTTCACATA 517149
Qy 262 -----GlyThrValSerH1aserAla11eAenLeuGlyThreSerAlaYs11eThrAla 280
Db 517148 CACCAACAACTACGAAAGAAATTTATTAAGACATAGATCTACGCAAGATACAGAAAT 517089
Qy 280 eAenGlyAla11eGlnGlyH1eThr11eYrPheYrAenPro11eThrValThnGlySerT 300
Db 517088 TACGTGCAATATCTGGGACATAGATCTTTTCTACATCGAATACGTAATACGGCGT 517029
Qy 300 hSerValAlaAenPheAenAen11eAenSerProAenPheThrGlyAenAenlyeGlyYrT 320
Db 517028 CGGATTTCTACATATCTTAAATCTCAATTAAGCTGATGACAGTAAATAGTACAGATTA 516969
Qy 320 hGlyThr11eVal11ePheSerGlyYglYleuThnGlnAglYalYleAenPglYulYrA 340
Db 516968 GTGGGTGATGTTTCTTCTGGGAAAGCTCTCTAAGATGAAAGCAAGTTGACAGACA 516909
Qy 340 eAenGlyThreSerlyeLeuGlnAenValAlaAenlyeAenGlyThrVal11eValLeuYsG 360
Db 516908 ACCTGACTTCTACGCGAGGACGCTGTAACCTACGACAGAAATTTAGTACTTAAAC 516849
Qy 360 lyAenValYalLeuSerAlaAenGlyPheSerGlnAenPheAenSerlyeLeu11eMecA 380
Db 516848 GTGGTGTCACTCTGATACGAAAGGCTTTACTCAGACCGCGGTTCTCTGTTATATAG 516789

Qy 380 ePLeuGlyThreSerleuValAlaenThnGlnuser11eGlnLeuThrAenLeuGln11eA 400
Db 516788 ATCGGCGACACAGCTTAACCAAGTACAGAGAGGTCACTTAAACAGTCTTCCATTC 516729
Qy 400 eN1eAenSerLeuAenGlnGlyYleYs11eYsLeuSerAla11eThrAlaGlnYrA 420
Db 516728 CTGTAGACTCTTTAGCGAGGGTAAAGAAAGTTGATATGCTGCTTCTCAGCAAGTAA 516669
Qy 420 eP11eAenGlyAenAenPheProVal11eA11eSerAenPgluserPheYrGlnAen 440
Db 51668 ATGTAGCCCTTAGGTGCTCCAGATCTTCTTTGATACCAAGGAAATCTTATGAATC 516609
Qy 440 lyPheLeuAenGlnAenPhe11eSerYrAenGly11eLeuGlnLeuAenPheAenPhe 460
Db 516608 ACAGCTTACGAAAACTCAAGACTT---TCATTTGTGACACTCTGCT---CTGGGTA 516555
Qy 460 leVal11eSerAlaAenPheSerAenSer11eAenPheAenValGlnSerPro-----YrGlyT 478
Db 516554 CTGCAACAACATACAGATGTTCCAGCGGTTCTTACAGTACCAACTCTCAGCACTATGGGT 516495
Qy 478 YrGlnGlyYleThrPheAenThrPheAenPheAenPheAenPheAenPheAenPheAen 492
Db 516494 ATCAAGTACTTGGGAAATGACTTGGGTTGATGATACCGCAAGCACTCCAAAGACTAAGA 516435
Qy 492 yEalAenThrValSerThrAlaYsglnSerPheAenProThrAlaGlnGlnAalAenProl 512
Db 516434 CAGGCACTTACCTTGGACCAATACGGGCTACCTTCGAAATCTGAGGCTCAAGGACCTT 516375
Qy 512 eUValProAenLeuLeuThrPglYserPhe11eAenPheAenPheAenPheAenPhe11eG 532
Db 516374 TAGTTCCTAATAGCTTGGGATCTTTTTCAGATCCAAACGATTCAGGCTGATCAGT 516315
Qy 532 lyLeuGlyThnGlnGlyAlaProYrGlnYrAenPheThrValAalagly11eSerAenV 552
Db 516314 AGAGAGGCTTGTGACTTGTTCAGATCAGAGCTTGTGGCTGCGGAGTGGCAAT 516255
Qy 552 a11eH1eAenSerGlyAenGlnAenGlnAenGlnAenGlnAenGlnAenGlnAenGlnA 572
Db 516254 TCTTATGATTAAGATTAAGAAAGGCAAAACCAATACCGTATCAATCTGATGATATG 516195
Qy 572 a1ValGlyAlaSerThrAenPheProGlyYrAenPheThreuserLeuGlyPheAalGlnL 592
Db 516194 CTATCGAGGAGTACAGGCACTTGTCTGAAATCTTAATTAATGCTTTCCTTTCCACAC 516135
Qy 592 eUPhaAlaAenPheAenPheYrPheMetAenThrAenPheAalAenThrYrAlaGlys 612
Db 516134 TCTTGTGATGCAATTAAGATTTCTTAGTGGCTAAATCAATCAATCAATCAATCAATCA 516075
Qy 612 eThreAenGlnGlnH1eAenPheAenPheAenPheAenPheAenPheAenPheAenPhe 632
Db 516074 CCTTATATATCAACACATTCACAGATATGATGAGGTTGATAGTGTCTCTTAAATTA 516016
Qy 632 lyGlyLeuAenGlnL1eLeuLeuProYrValSerlyeThreuserProCyserPheYrG 652
Db 516015 -----CTTCTGCTCTTGGAGTCAATTAACCTCTGTTTAAAG 515976
Qy 652 lyGlnLeuserYrGlyH1eThrAenPheAenPheAenPheAenPheAenPheAenPheAen 672
Db 515975 GGCACCTGCTTATAGCAACGTCAGTAATGATCTTAAGACAAAGTAACTCTGCTATCTCG 515916
Qy 672 roProThreuserThrAenPheAenPheAenPheAenPheAenPheAenPheAenPhe 692
Db 515915 AGGTC-----AAAGTCTTGGGGAATTAATGCTTTTAAACATGATGTTGG 515871
Qy 692 lyThrAenValAlaValGlnAenThrSerGlyAenGlyPhe-----P 706
Db 515870 GA-----GCTTCTTCTCATCTTATCTGAAATCACTGATGTT 515832
Qy 706 hGlnGlnGlyThrProPheValYsValGlnAlaValYrAlaAenPheAenPheAenPheV 726
Db 515831 TTAGATACCTATGCTCATACATCAACATGAAATCTGACCTATATATAGTACGACGACTCT 515772

QY	726	algluLengLlVAlalleSerAaPheSerAaPheSerHisLeuTYrAsnLeuAlAlIleP	746
Db	515771	CGGAAAGGTACAGAGGAAGATCTTTGATGACAGCAACTCTTCAAATTATCTTTGC	515712
QY	746	roLeuGLYlIleLeuGLuLulYsArGPheAla-----GIuInTYrTYHleValY	763
Db	515711	CTATAGGGGTGAAGTTTGAAGG---TTCTCGATTGTATATGACTTTTCTTATGATCTGA	515655
QY	763	aAlaIaMeTYrSerProAaPValCYaArSerAaAProLYsCYrThrThrThrLeuLeuS	783
Db	515654	CTTATATCTTAATGTTCTGATCTTATCCGCAATGATCCCAATGACCTACAGCACTTGTA	515595
QY	783	erAaenGLInGLYSerTlPbYrThrLYsGLYSerAaLeuAlAaArgInAlaGLYlIleValG	803
Db	515594	TCAGCGGAGCCTCTTGAGCAACTTATGCCAATAACTTACACAGCAGGCTTGCAAGTGC	515535
QY	803	InAlaSerGLYpHeArSerLeuGLYAlAlAlaGLuLeuPheGLYAsnPheGLYpHeC	823
Db	515534	GTGCGGAGATCACTACGCTTCTCTCTTAATGTTTGAAGCTCGGCGCAGTTGTCTTTG	515475
QY	823	IuTlPArGLYSerSerArGLYSerTYrAsnValAspAlaGLYSerLYsIleLYsPhe	841
Db	515474	AAAGTTCTGGATCTCCACGAGATTATATGTAGATCTTGCGGGTAAAGTTCCAATTC	515419

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US-09-556-877-182
Sequence 182, Application US/09556877
Patent No. 6432916
GENERAL INFORMATION:
APPLICANT: Peter
APPLICANT: Probat, Peter
APPLICANT: Bhatia, Ajay
APPLICANT: Skeiky, Yashir
APPLICANT: Piling, Steve
APPLICANT: Malsomeuve, Jeff
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
FILE REFERENCE: 210121.469C5
CURRENT APPLICATION NUMBER: US/09/556,877
CURRENT FILING DATE: 2000-04-19
NUMBER OF SEQ ID NOS: 305
SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
SEQ ID NO 182
LENGTH: 3021
TYPE: DNA
ORGANISM: Chlamydia
US-09-556-877-182

Alignment Scores:
Pred. No.: 5,22e-91 Length: 3021
Score: 939.00 Matches: 285
Percent Similarity: 39.77% Conservative: 127
Best Local Similarity: 27.51% Mismatches: 334
Query Match: 21.86% Indels: 290
DB: 4 Gaps: 29

US-09-830-446-27 (1-841) x US-09-556-877-182 (1-3021)

QY 36 PhaaapGClYThrThrSerThrThrSerPheSerSerLyvThrSerSerAlaThraapGly 55
Db 91 TACGAATGGGAGACGTTAACTGATCATTTCCCTTAAGTATTAAGAGATCCAGATGGG 150
QY 56 ThcAsnTyvAlPhelybaaSerValIleGluAnValPProLyvThrGlyGluThr 75
Db 151 ACTACTGTTTTTCTCGACAGAGAGTTAACTTAAAAATCTTGACAACTTCAATGGAGCT 210
QY 76 GlInSerThSerCyapbelybaaSerAlaAlaIleGlyAspLeuAnPheLeuGlyGly 95
Db 211 TTGCCTTAAAGTGGTTTGGGAAC-----TTATTAGGGAAGTTTACTGTTTAGGAGA 264
QY 96 GlYPhaaSerPheThrPheSerAnIleapAlaThrThrAlaSerGlyAlaAlaIleGly 115
Db 265 GGAACACTCGTTGACTTTGAGAAACATA--CGAACTTCAAAATGGGCGAGCTTAAGT 321

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OY		116	tergluaialaaenlyThrValThreuserglyPheSerAlaleusPhe-----	133
Dd		322	AATAGCGCTGATGACTGTTCATTACATTGAAGGTTTAAAGATTATCTTTCCATT	381
OY		134	-----LeuysSerPro	137
Dd		382	TGCATTCACTACTGCCGTACTGCCGTGTCAGCAAGCTAATAAAGGTAGCCAGACTCCG	441
OY		138	AlaseThrValThraenglyleuglyalialeanvalylgylAsnleuserleu	157
Dd		442	ACGACAACTATCACCCGCTCTAATGGTACTATTTCCTAAAACAATCTTTTGTTACTC	501
OY		158	AspaAnaPyrsValLeuIleGlinaBpaNpheSerThrglyASPglylalailean	177
Dd		502	AATATGAGAAGTTCTCATTTCTATAGTAATTTTAGTCTGGAGATGGGGAGCTATAGAT	561
OY		178	CysAlaglySerLeuyle-----	184
Dd		562	---GTTAAGACTTAAAGGTTCAAGAAATTAGCAAGCTTTGTCTTCCAAGAAATACT	618
OY		185	-----AlaBpaAn	187
Dd		619	GCTCAAGCTGATGGGGAGCTTGTCAATAGTCAACAGTTTCTGTCTATGCTAACGAG	678
OY		188	LysSerLeuserPheIleglyAsnsereserThraArglyAlaIleHsth---	206
Dd		679	GCTCCTATTTGCTTTGTATGCGAATGTTCAAGAGTAAAGGGGGAGATTGCTGCTGTT	738
OY		206	-----	206
Dd		739	CAGATGGGACAGGAGAGTGCATCATCTACTTCAACAAGATCCAGTAACTTT	798
OY		206	-----	206
Dd		799	TCCAGAAATACCTGCGTAGATTGTGATGGAACTPA GCCAGTAGAGAGAGGATTTAC	858
OY		207	----LysBaenLeuthLeuserSerylglyuThrleuPheglnglysenThrala	224
Dd		859	TCCTACGGGAAGCTTGCTTCTCTGAATATAGAAAAACCCTTGTCTCAACATGTTGCT	918
OY		225	-----Prothr	226
Dd		919	TCTCTGTTTACATTTGCTGCTAAGCAACCAACAAGTGAAGAGGCTTTCTAATACAGTAAT	978
OY		226	-----	226
Dd		979	AATTACGAGATGAGAGAGCTATCTTCTGTAAGATGGCGCAAGCAGATCCAATAAC	103
OY		227	-----AlaIaIa	228
Dd		1039	TCTGGATCAGTTCTCTTGATGAGAGAGGAGTAGTTTTCTTATAGACATGTAGCTGCT	109
OY		229	GLylys-----	230
Dd		1099	GGGAAAGGGGAGACTATTATGCCCCAAAAGCTCTCGGTTGCTAACTGSCCCTGTACA	115
OY		231	-----GlyglyAlaIleAlaIleAlaasPserglyThrleu	242
Dd		1159	TTTTTAAAGAAATTCGCTAATGATGATGTGAGAGATTATTTAGAGAAATCTGGAGAGCTC	121
OY		243	SerIleSerglyaspserglyaspIlellepehgugly-----	255
Dd		1219	AGTTTATTCGCTGATTATGAGAGATTTATTTTCGATGGGAATCTTAAAGAACACGCCAA	127
OY		256	---AsnthrlIeglyAlaethrgly---ThrValaserHiserAlalleapreuglyThr	273
Dd		1279	GAGAAATGCTCCGATGTTAATAGGCTTAACGTGTCTCAACAAGCAATTCAGATGGGATCG	133
OY		274	SeralalyllernAlaIeuarqAlaIaglInglyHsthrIleTyRPhetyrasPpro	293
Dd		1339	GGAGGGAAATATACACATTTAAGAGCTAAAGAGGCAATCAGATTCTCTTAAATATATCC	139
OY		294	IleThrVal---ThrglySerThserValAlaapala-----Leuanlleaen	309

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Db      1399 ATCGAGATGGGAAAGAAATTAACGACGCGAGCTTCCAACTCTAAATTAAC 1458
Qy      310 SerProapThrGlyAspAsnLysGlyThrGlyThrIleValPheSerGlyGluLys 329
Db      1459 -----GATGGTGAAGATACACAGCGGATATTGTTTGGCT----- 1494
Qy      330 LeuThrGluAlaGluAlaLysAspGluLysAsnArgThrSerLysLeuGlnAsnVal 349
Db      1495 -----AATGAAAGCATCTTGTGACCAAAATGTT 1524
Qy      350 AlaPheLysAsnGlyThrValAlaLeuLysGlyAspValValLeuSerAlaAsnGlyPhe 369
Db      1595 ACGATAGAGCAAGAGAAAGATCTTCTCGTGAAGCAAAATTAATCAAGTAATCTCTCA 1584
Qy      370 SerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu----- 385
Db      1585 AGTCAGACAGCGTGAGGT---CTGTATATGGAAGCTGGGAGTACATTGGATTGTAACT 1641
Qy      386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
Db      1642 CCACAAACCAACCAACAGCTCTCCGCTAATCAAGTATACAGCTTTCACATCTGCAT 1701
Qy      399 IleAsnIleAspSerLeuArgAsnGlyLysLysIle----- 410
Db      1702 TTGTCTCTTCTCTTGTGTAGCAAAACATGACAGTTCATCCTCAATCTCTCA 1761
Qy      411 -----LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
Db      1762 GCGCAAGATCTTCATCTGCACTGATGTTGTTGACACAACTGCTGTTCTTCAATAGT 1821
Qy      425 ArgProValValLeuAlaIleSerAspGluSerPheThrGlnAsnGlyPheLeuGln 444
Db      1822 GGGCTATCTTTTGGAGATTGATGATACAGCTTATGATAGC----- 1866
Qy      445 AsnHisSerTyrAsp-----GlyIleLeuGluLeuAspAla 456
Db      1867 -----TATGATTTGGCTAGGTTCTATCAAAAATCAATGCTCTGAATTAACGTTA 1917
Qy      457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro-- 475
Db      1918 GGGACTAAGCCCGCCAGCTAATGCCCATCATGATTGACTCTAGGGAATGATGCTTAAG 1977
Qy      476 TyrGlyTyrGlnGlyLysThrThrIleAsnTyrPserThrAspAspLys----- 491
Db      1978 TATGGCTATCAAGAGCTGGAAGCTTGGCTGGAGTCTTAATACAGCAAAATATGCTCT 2037
Qy      492 -----LysAlaThrValSerTyrAlaLysGlnSerPheAsnProThrAlaGln 508
Db      2038 TATACTCTGAAAGCTACA-----TGACTTAAATCGGATATATCTCGGCTTAGCA 2091
Qy      509 GluAlaProLeuValProAsnLeuLeuTyrGlySerPheIleAspValArgSerPheGln 528
Db      2092 GTAGCTCTCTTGGTTCAAATAGTTATGGGATCATATTGATATGATCATGCTGGCAT 2151
Qy      529 AsnPheIleGluLeuGlyThrGluGlyAlaProTyrGluLysArgPheThrValAlaGly 548
Db      2152 TCAGCAATTCAGCAAGCTGATGGGCGCTCTTATTTGTCAGAGATTAAGGTTCTCGA 2211
Qy      549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgIleValSer 568
Db      2212 GTTTCGAATTTCTTCATCATACACCGCATGCTTTAGTCAGAGATATCGCATATTAAT 2271
Qy      569 GlyGlyAlaValAlaGlyLysThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
Db      2272 GGGGGTATTCCTTAGACCAATCTCTACTT---GATCATCATGATGTTTGGTCTAGCA 2328
Qy      589 PheAlaGluLeuPheAlaArgAspLysAspTyrPheMetAsnThrAsnPheAlaLysThr 608
Db      2329 TTACCGAAGATTTGCTGATTTAAAGATTAATGTAAGTGTGCTGCTCAATCATATGCT 2388
Qy      609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrSerValIleSerIleLeu 628

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Db      2389 TGCAATAGATCCGTTTATCTATCTAACCAACAGCTTATGNGA-----TCTATTGG 2442
Qy      629 LeuGlyGluGlyLysLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648
Db      2443 TTCGAGATGGCTTATCCGT----- 2463
Qy      649 SerPheTyrGlyGlnLeuSerTyrGlyHisThrAspHisArgMetLysThrGluSerLeu 668
Db      2464 -----GCTAGCTACCGGTTTGGGAATCAAGATTAACCACTCATAT--- 2505
Qy      669 ProProProProThrThrLeuSerThrAsp---HisThrSerTyrGlyTyrValTyrP 687
Db      2506 -----ACATTTGCAGAGAGAGCGCATTCGATGTTCTGTTGGAATAAATCTGTG 2550
Qy      688 AlaGlyGluLeuGlyThrArgValAlaValGluAsnThrSerGlyArgGlyPhePheGln 707
Db      2551 GCTGAGAGATTGAGCGGAGATTACCGATTGATGATTCTTCAATCACTTAACCTCAATTGAAT 2610
Qy      708 GluTyrThrProPheValIleValAlaValTyrAlaArgGlnAspSerPheValGlu 727
Db      2611 GAGTGGCTCTCTTCTGTCACAGCTGAGTTTCTTATGCCATCATGATCTTTTACAGAG 2670
Qy      728 LeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeu 747
Db      2671 GAAGCGCATCAAGCTCGGCGCATTCMAAGCGGACATCTCTTAATCTATCATGCTCTGTT 2730
Qy      748 GlyIleLysLeuGluLysArgPheAla-----GluGlnTyrTyrHisValValAlaMet 765
Db      2731 GAGAGGAATTTGATGATGATGTTTCTAGTACACATCTTAATAATATAGCTTTATGGCGCT 2790
Qy      766 TyrSerProAspValCysArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGln 785
Db      2791 TATATCTGATGCTTATACGACCATCTCTGTAAGTACAGAACCTCTCTATCCATCA 2850
Qy      786 GlySerTyrLysThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805
Db      2851 GAGACATGACAAACAGATGCTTTCATTTAGCAAGACATGAGTGTGGTTAGAGAGATCT 2910
Qy      806 GlyPheArgSerLeuGlyAlaAlaValLeuPheGlyAsnAsnPheGlyPheGluTyrParg 825
Db      2911 ATGTATGCTTCTCTCAACAGATATATAGATATATAGATATATGCGCATGAGATATGATGCA 2970
Qy      826 GlySerArgSerTyrAsnValAspAlaGlySerLysIleLysPhe 841
Db      2971 GATGCTTCTCAAGCTATGCTTATGATGTCAGAGATTAAGTCCGCTTC 3018

RESULT 4
US-09-620-412C-182
; Sequence 182, Application US/09620412C
; Patent No. 6448214
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 182
; LENGTH: 3021
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-182

Alignment Scores:
Pred. No.: 5,226-91
Score: 939.00 Length: 3021
Percent Similarity: 39.77% Matches: 285
Best Local Similarity: 27.51% Conservative: 127
Query Match: 21.86% Mismatches: 334
DB: 4 Indels: 290
Gaps: 29

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US-09-830-446-27 (1-841) x US-09-620-412C-182 (1-3021)

QY 36 PheAspGlyThrThrSerThrThrSerSerSerLeuThrSerSerAlaThrAspGly 55
 Db 91 TACGATGGGAGACGTTACCTGATCATTTCCCTATACGTTATAGAGATCCGAGCTGG 150
 QY 56 ThrAsnValPheLeuAspSerValValIleGluAsnValProLeuThrGlyLeuThr 75
 Db 151 ACTACGTTTTTTCGACAGAGAGTTACATTAATAAAATCTTGACAATCTATGACGT 210
 QY 76 GlnSerThrSerCysPheLeuAsnAspAlaAlaIleGlyAspLeuAsnPheLeuGly 95
 Db 211 TTGCTTTTAGTGTGTTGGGAACTTTATAGGAGTTTACTGTTTAGGGAGA 264
 QY 96 GlyPheSerPheThrPheSerSerAlaAlaPheThrAlaSerGlyAlaAlaIleGly 115
 Db 265 GGAACACTGTTGACTTTCAGAAACATA---CGGACTTCAAAATGGGCGAGCTCTAAGT 321
 QY 116 SerGluAlaAlaAsnLeuThrValThrLeuSerGlyPheSerAlaLeuSerPhe----- 133
 Db 322 AATAGCGCTGCTGATGAGCTGTTACTATTTAGAGGGTTTAAAGAAATTAATCTTTCCAA 381
 QY 134 -----LeuYsSerPro 137
 Db 382 TGCATATTCATTACTTGCCTGACTGCTGTCAGACGATATAGGGTATGCCAGCTCCG 441
 QY 138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuLeu 157
 Db 442 ACGACAACTCTACACCGCTATATGCTATATTTATCTTAAACAGATCTTTGTATAC 501
 QY 158 AspAsnAspLeuValLeuIleGlnAspAsnPheSerThrGlyAspGlyAlaIleAsn 177
 Db 502 AATATAGAAAGTCTCATCTCTATTAAGTATTTAGTCTCGAGATGGGAGCTATTAAGT 561
 QY 178 CysAlaGlySerLeuValLeu----- 184
 Db 562 ---GCTAAGAGCTTAACGGTTAAGAAATTAAGCAAGCTTTGTCTTCCAGAAATTA 618
 QY 185 -----AlaAsnAsn 187
 Db 619 GCTCAAGCTGATGGGAGCTTGTCAAGTATGATCAACGATTTCTGCTATATGCTTAACGAG 678
 QY 188 LysSerLeuSerPheIleGlyAsnSerSerSerThrAlaGlyAlaIleHisThr----- 206
 Db 679 GCTCTATATGCTTTGTACGAAATGTTCAGAGATAGAGGGAGGATGCTGCTGTT 738
 QY 206 ----- 206
 Db 739 CAGGATGGCAGACAGAGATGTCATCATCTTAACAAGAAATCCAGTATGAATTT 798
 QY 206 ----- 206
 Db 799 TCAGAAATATACGCGTAGAGTTTGAATGGAAAGTACCCGAGTAGAGAGGAGATTAC 858
 QY 207 -----LysAsnLeuThrLeuSerSerGlyGlyLeuThrLeuPheGlnIleAsnThrAla 224
 Db 859 TCCTACGGGACGCTGCTTCTCTGAATTAATGAAAAACCTTGTCTCAACAATGTGCT 918
 QY 225 -----ProThr----- 226
 Db 919 TCTCTGTTTACATTCGCTGCTAAGCAACCAACAGATGACAGGCTTCTAATACGATAT 978
 QY 226 ----- 226
 Db 979 AATTACGAGATGAGAGACTATCTTCTGAAGATGATGCGACAGAGATCCAAATAC 1038
 QY 227 -----AlaAla 228
 Db 1039 TCTGATCACTTCTCTTGAATGAGAGAGATGTTTCTTATAGCAATGTAAGCTGCT 1098
 QY 229 GlyLys----- 230
 Db 1099 GGGAAAGGGGAGCTATTTATGCAAAAAGCTCTGGTTGCTAATCTGGCCCTGTACAA 1158

QY 231 -----GlyGlyAlaIleAlaIleAlaAspSerGlyThrLeu 242
 Db 1159 TTTTAAAGAAATATGCTTATATATGATGGAGCGATTTATTTAGAGAAATCTGGAGACTC 1218
 QY 243 SerIleSerGlyAspSerGlyAspIleIlePheGlnGly----- 255
 Db 1219 AGTTATATCGCTGATTAATGAGATATATTTTCATGGGAATCTTAAGAAACAGCCAAA 1278
 QY 256 ---AsnThrIleGlyAlaThrGly---ThrValSerHisSerAlaIleAspLeuGlyThr 273
 Db 1279 GAGAAATGCTGCCGATGTTAATGCGTAATCTGTCTCTCAACAGCAATTCGATGGGATG 1338
 QY 274 SerAlaValIleThrAlaLeuAsnGlyAlaIleGlnIleHisThrIleCysPheThrAspPro 293
 Db 1339 GAGGAGAAATATACACATTAAGCTTAAGAGCTAAAGAGGCGATCAAGATCTCTTAATATGCC 1398
 QY 294 IleThrVal---ThrGlySerThrSerValAlaAspAla-----LeuAsnIleAsn 309
 Db 1399 ATCGAGATGCGAAAGAAATACACAGCCGCGAGCTCTCCAAATCTTAATAAATTAAC 1458
 QY 310 SerProAspThrGlyAspAsnLeuGlyThrGlyThrIleValPheSerGlyLeuLys 329
 Db 1459 -----GATGCTGAGAGATACACAGGGGATATGTTTCT----- 1494
 QY 330 LeuThrGluAlaGluAlaValAspGlyLysAsnArgThrSerLeuLeuGlnAsnVal 349
 Db 1495 -----AATGAAAGAGTACTTTGACAAAATGT 1524
 QY 350 AlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGlyPhe 369
 Db 1525 ACGATATAGCAAGAAAGATGTTCTTCTGTAAGAAAGCAAAATTAATCACTGAATCTCTA 1584
 QY 370 SerGlnAspAlaAsnSerLeuIleLeuAspLeuGlyThrSerLeu----- 385
 Db 1585 AGTCAGACAGTGGAGT---CTGTATATGAAAGCTGGGAGTACATGATTTGTA 1641
 QY 386 -----ValAlaAsnThrGlySerIleGluLeuThrAsnLeuGlu 398
 Db 1642 CCAGAACACCAACAAACGCTCTGCCCTAATCAGTTGATCAACGCTTCCAAATGCA 1701
 QY 399 IleAsnIleAspSerLeuArgAsnGlyLysValLeu----- 410
 Db 1702 TTGCTCTTTCTTTCTTTGTACCAACAATGCAATGCAATCTCTCAACATCTCCA 1761
 QY 411 -----LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
 Db 1762 GCGCAAGATTCATCTGACAGTCACTGTTGATACACAACTGCTGTTCTGTACAAATTA 1821
 QY 425 ArgProValValLeuAlaIleSerAspGlySerPheIleGlnAsnGlyPheLeuAsnGlu 444
 Db 1822 GGCCTATCTTTTGGAGATTGGATGATACAGCTTAATGATAGG----- 1866
 QY 445 AspHisSerThrAsp-----GlyIleLeuGluLeuAspAla 456
 Db 1867 -----TATGATTTGGCTAGCTTCTAATCAAAAATCAATGCTCTGAATTTACGTTA 1917
 QY 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475
 Db 1918 GGGACATAGCCCGCCAGCTAATCCCATCAGATTTGACCTAGGGAATAGATGCTTAAG 1977
 QY 476 TyrGlyTyrGlnGlyLysThrIleAsnThrPheSerThrAspAspLys----- 491
 Db 1978 TATGCTATCAAGGAGCTGGAAGCTTGCTGTGGATCTCAATACAGCAATATATGCTCT 2037
 QY 492 -----LysAlaThrValSerThrAlaLysGlnSerPheAsnProThrAlaGln 508
 Db 2038 TATACTCGAAAGCTACA-----TGAATTAATCTGGATTAATCTGGCTAGACCA 2091
 QY 509 GlnAlaProLeuValProAsnLeuLeuThrGlySerPheIleAspValArgSerPheGln 528
 Db 2092 GTAGCTTCTTGTCTTCAAAATGATTTATGGGAGATCAATTTATGATATAGATCTGGCAT 2151

QY 207 -----LysAsnLeuThrIleuSerSerGlyGlyIuThrIleuPheGlnGlyAsnThrAla 224
 |||:::|
 Db 859 TCCTACGGGAACGTTGCTTCTCGAATAATAGGAAAAACCTGTTTCTCAACAATGTTGCT 918
 QY 225 -----ProThr----- 226
 |||
 Db 919 TCTCTGTTTACATTGCTGTGAACCAACCAAGTGAAGAGGCTTCTAATACAGTAAT 978
 QY 226 ----- 226
 Db 979 AATTACGAGATGAGAGAGCTAATCTTGTAAAGATGTCGACAGAGATCCAAATAC 1038
 QY 227 -----AlaAla 228
 |||
 Db 1039 TCTGATCAGTTTCCTTATGAGAGAGAGTGTTCCTTAGTACAAATGAGCTGCT 1098
 QY 229 GlyLys----- 230
 |||
 Db 1099 GGGAAAGGGGAGCTATTATGCAAAAGCTCTCGTTGCTAATGTCGCTGTACAA 1158
 QY 231 -----GlyGlyAlaIleAlaIleAlaIleAspSerGlyThrIleu 242
 |||:::|
 Db 1159 TTTTAAAGAAATATCGCTAATGATGTGGAGCAATTTATTAGAGAAATCTGAGAGCTC 1218
 QY 243 SerIleSerGlyAspSerGlyAspIleIlePheGlnGly----- 255
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 Db 1219 AGTTATCTGCTGATTAATGAGATATTTATTTGATGGAAATCTTAAAGAACGCCAA 1278
 QY 256 ---AsnThrIleGlyAlaThrGly-----ThrValSerHisSerAlaIleAspLeuGlyThr 273
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 Db 1279 GAGAAATGCTCCGATGTTAATGCGCTAATGCTGTCTCCACAAAGCTTTCATGGAGATCG 1338
 QY 274 SerAlaIleIleThrAlaIleuArgAlaAlaGlnGlyHisThrIleIleTyrrPheTyrrAspPro 293
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 Db 1339 GAGGAGAAATTAACGATTAAGAGCTTAAGAGCGGATCAGATTCCTTTAATGATCC 1398
 QY 294 IleThrVal---ThrGlySerThrSerValAlaAspAla-----LeuAsnIleAsn 309
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 Db 1399 ATCGAATGCGCAACGGAATTAACGACCGACGCTCTCCAACTCTTAAATTAAC 1458
 QY 310 SerProAspThrGlyAspAsnLysGlyTyrrThrGlyThrIleValPheSerGlyGlyLys 329
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 QY 330 LeuThrGluAlaGluAlaLysAspGlyLysAspArgThrSerIleLeuLeuGlnAsnVal 349
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 Db 1495 -----AATGAAAGCAGTACTTGTATCAAAATGTT 1524
 QY 350 AlaPheLysAsnGlyThrValValIleuLysGlyAspValValIleuSerAlaAsnGlyPhe 369
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 QY 370 SerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerIleu----- 385
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 Db 1585 AGTCACAGACAGGTGGAGT---CTGTATATGGAAGCTGGAGTACATTTGTAATCT 1641
 QY 386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGln 398
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 Db 1642 CCAACAACACACACAGCTCTCGCTAATCAAGTATCAAGCTTTCATCTGCAT 1701
 QY 399 IleAsnIleAspSerLeuArgAsnGlyLysIle----- 410
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 Db 1702 TTGTCTCTTCTTCTTGTGTAACAAATGCAATTCGATCTCTCAATCTCTCA 1761
 QY 411 -----LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
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 Db 1762 GCGCAAGATTCATCTGATCTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1821
 QY 425 ArgProValValIleuAlaIleSerAspGlySerPheTyrrGlnAsnGlyPheLeuAsnGln 444
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 Db 1822 GGGCCATATCTTTTGAAGATTTGATGATGATGATGATGATGATGATGATGATGATGATGAT 1866
 QY 445 AspHisSerTyrrAsp-----GlyIleLeuGluLeuAspAla 456

Db 1867 -----TATGATTTGGCTAGGTTCTAATCAAAAAATCAATCTCTGAAATTAACAGTTA 1917
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 Db 1918 GGGACTAAGCCCCAGCTAATGCCCATCAGATTTGATCTTGAAGAAATGATGCTTAAG 1977
 QY 476 TyrGlyTyrrGlnGlyLysTyrrPheThrIleAsnTyrrSerThrAspAspLys----- 491
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 Db 1978 TATGCTATCAAGAGAGCTGGAAGCTTGGGTGGATCTTAATCAGCAAAATATGATGCT 2037
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 Db 2038 TATACTCGAAGCTACA-----TCGACTAATACTGGATATATCTCGGCTGAGCGCA 2091
 QY 509 GluAlaProLeuValProAsnLeuLeuTyrrGlySerPheIleAspValArgSerPheGln 528
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 Db 2092 GTAGCTTCTTGGTTCCAAATGATTATGGGATCCATTTAATATACAGATCTGCGCAT 2151
 QY 529 AsnPheIleGluLeuGlyThrGlnGlyAlaProTyrrGlyLysArgPheThrPalAlaGly 548
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 QY 549 IleSerAsnValIleuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSer 568
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 Db 2212 GTTTCGAATTTCTTATCATATGACCGCATGCTTATGATCAGGAGATATCGTATATTAAT 2271
 QY 569 GlyGlyAlaValAlaGlyLysThrArgMetProGlyGlyAspThrIleuSerLeuGly 588
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 Db 2272 GGGGGTTATCTCTTACAGCAAACTCTACTTT---GATCATCATGATGTTGGCTAGCA 2328
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 QY 609 TyrAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrrSerValIleLeu 628
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 Db 2506 -----ACATTTGAGAGAGAGAGGATGTTGTTGGATATAATCTGCTG 2550
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 Db 2791 TATATCTGATGCTTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2850
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QY 386 -----ValAlaAnthGluSerIleuLeuThrAsnLeuGlu 398
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QY 399 IleAsnIleAspSerIleuArgAsnGlyLysIle----- 410
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    1630 TTGTCTCTTCTCTCTTGTGTAGCAACATGCAATTGCAATCTCTTACCAATCTCCA 1689
QY 411 -----LysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAsp 424
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    1750 GGGCTTATCTTTTGTGAGATTGATGATACAGCTTATGATAG----- 1794
QY 445 AspHisSerTyrlAsp-----GlyIleLeuGluLeuAspAla 456
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QY 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475
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    1846 GGGACATGAGCCCGACGATATGCCCCATCAGATTGATCTAGGAGATGAGATGCCCTAG 1905
QY 476 TyrlGlyTyrlGlnGlyLysTyrlThrIleAsnTyrlSerThrAspLys----- 491
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    1906 TATGGCTATCAGAGAGCTGAGAGCTGCGGGATCTCTTACAGCAAAATTAATGCTCT 1965
QY 492 -----LysAlaThrValSerThrAlaLysGlnSerPheAsnProThrAlaGlnGlu 508
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    1966 TATACTCTGAAAGCTACA-----TGCACCTAAACCTGGATATATCTGGAGCTGACGA 2019
QY 509 GluAlaProLeuValProAsnLeuLeuTyrlGlySerPheIleAspValArgSerPheGln 528
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QY 529 AsnPheIleGluLeuGlyThrGlnGlyAlaProTyrlGluLysArgPheTyrlValAlaGly 548
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QY 569 GlyGlyValAlaValGlyAlaSerThrArgMetProGlyLysAspThrLeuSerLeuGly 588
    |||||
    2200 GGGGTTATCTCTTGAAGCAAACTCTACTTT---GATCATCATGATGTTGGCTTAGCA 2256
QY 589 PheAlaGlnLeuPheAlaArgAspLysAspTyrlPheMetAsnThrAsnPheAlaLysThr 608
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    2257 TTACCGCAAGATATTTGTAGATCTAAAGATTAATAGTGTGCTCATCATCATGCT 2316
QY 609 TyrlAlaGlySerLeuAspGlnHisAspAlaSerLeuTyrlSerValIleSerIleLeu 628
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    2317 TGCATAGGATCCGTTTATCTATCATCCCAACAGCTTAAATGTGA-----TCTATATTG 2370
QY 629 LeuGlyLysIleuArgGluIleLeuLeuProTyrlValSerLysThrLeuProCys 648
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QY 649 SerPheTyrlGlyLysLeuSerTyrlGlyLysThrAspHisArgMetLysThrGluSerLeu 668
    |||||
    2392 -----GCTACCTACGGGTTTGGGAATCAGCATTAAGAACTCATAT--- 2433
QY 669 ProProProProProThrLeuSerThrAsp---HisThrSerTyrlGlyLysTyrlValTyr 687
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QY 708 GluTyrlThrProPheValLysValGlnAlaValTyrAlaArgGlnAspSerPheValGlu 727
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    2539 GAGTTCGCTCTTTCGTGCAAGCTGAGGTTTCTTAAGCCATCATGATCTTTTACAGAG 2598
QY 728 LeuGlyValAlaIleSerArgAspPheSerAspSerHisLeuTyrlAsnValAlaIleProLeu 747
    |||||
    2599 GAAGCGCATCAACCTGGCGATTCMAAGCGACATCTCTTAATCTATCATGCTCTGTT 2658
QY 748 GlyIleLysLeuGluLysArgPheAla-----GluGlnTyrlTyrlHisValValAlaMet 765
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    2659 GAGCTGAAGTTTATGATGATGCTTCTAGTACATCATCTTAATATATATGCTTATGCGGCT 2718
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QY 786 GlySerTyrlPheThrLysGlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSer 805
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    2779 GAGCATGACACACAGATGCTTCTTATTCAGACATGAGAGTGTGTTAGAGATCT 2838
QY 806 GlyPheArgSerLeuGlyAlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyrArg 825
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QY 826 GlySerThrArgSerTyrlAsnValAspAlaGlySerLysIleLysPhe 841
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RESULT 7

US-09-620-412C-170

; Sequence 170, Application US/09620412C

; Patent No. 6448234

; GENERAL INFORMATION:

; APPLICANT: Steven P. Fling

; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND

; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION

; FILE REFERENCE: 210121.469CT

; CURRENT APPLICATION NUMBER: US/09/620,412C

; CURRENT FILING DATE: 2000-07-20

; NUMBER OF SEQ. ID NOS: 363

; SOFTWARE: FastSeq for Windows Version 3.0/4.0

; SEQ ID NO 170

; LENGTH: 2949

; TYPE: DNA

; ORGANISM: Chlamydia

US-09-620-412C-170

Alignment Scores:

Pred. No.:	1.06e-90	Length:	2949
Score:	936.00	Matches:	285
Percent Similarity:	39.67%	Conservative:	126
Best Local Similarity:	27.51%	Mismatches:	335
Query Match:	21.79%	Indels:	290
DB:	4	Gaps:	29

US-09-830-446-27 (1-841) x US-09-620-412C-170 (1-2949)

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QY 56 ThrAsnTyrlValPheLysAspSerValIleGluAsnValProLysThrGlyGluThr 75
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QY 76 GlnSerThrSerCysPheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGly 95
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 QY 116 SerGluAlaIleAsnIleThrValThrIleuSerGlyPheSerAlaIleuSerPhe----- 133
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 Db 250 AATTAGCGCTGCTGATGAGACTGTTTACTATTGAGGGGTTTAAAGAAATTATCTTTTCCAAAT 309
 QY 134 -----LeuIleuSerPro 137
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 Db 310 TCCCAATTCACTTCCCTGCTGCTGCTGCAACGACTTAATAGGGTAGCCAGACTCCG 369
 QY 138 AlaSerThrValThrAsnGlyLeuGlyValAlaIleAsnValIleGlyAsnIleuSerLeu 157
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 QY 158 AspAsnAspIleValIleuIleGlnAspAsnPheSerThrGlyAspGlyValAlaIleAsn 177
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 Db 430 AATTAAATGAGAACTTCTCATTTACTAATTAATTAATTAATTAATTAATTAATTAATTAAT 489
 QY 178 CybAlaGlySerLeuIleu----- 184
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 QY 185 -----AlaAsnAsn 187
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 QY 188 LysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyValAlaIleIleThr--- 206
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 QY 206 ----- 206
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 QY 206 ----- 206
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 Db 727 TCCAGAAATACCTGCGTAGAGTTTGAATGGAAAGTACCCGAGTAGAGAGAGATTAC 786
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 QY 225 -----ProThr----- 226
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 QY 226 ----- 226
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 QY 227 -----AlaAla 228
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 QY 229 GlyLys----- 230
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 Db 1027 GGGAAAGGGGAGACTTATATGCSAAAAGCTGCTGCTGCTAAGTCTGAGCCCTGTAACA 1086
 QY 231 -----GlyGlyAlaIleAlaIleAlaIleAspSerGlyThrIleu 242
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 QY 569 GlyGlyAlaValAlaGlyAlaSerThrArgMetProGlyGlyAspThrIleuSerLeuGly 588
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Db	2317	TGCATGAGATCCGTTATCTATCTACCAACAAAGCTTATGNGA-----TCCATATTG	2370
Qy	629	Leuglgluglglglleuaglsuileuleuprottyrvalserlystheuprocys	648
Db	2311	TTCCGAGATGCGTTATTCGT-----	2391
Qy	649	SerPheTyrcylglnleuserTyrcylglnsthrasphlsargmetylethrgluserleu	668
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Qy	708	GlutyrtThrProPheValylvalglnalavalTyralargglnasersPheValgln	727
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US-09-598-419-170			
Sequence 170, Application US/09598419			
Patent No. 6565856			
GENERAL INFORMATION:			
APPLICANT: Skeiky, Yasir A.W.			
APPLICANT: Scholler, John			
TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND			
TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION			
FILE REFERENCE: 210121.469C6			
CURRENT APPLICATION NUMBER: US/09/598,419			
NUMBER OF SEQ ID NOS: 357			
SOFTWARE: FastSBQ for Windows Version 3.0/4.0			
SEQ ID NO 170			
LENGTH: 2949			
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ORGANISM: Chlamydia			
US-09-598-419-170			
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Score:	936.00	Matches:	285

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Best Local Similarity:	27.51%	Mismatches:	3358
Query Match:	21.79%	Indels:	250
DB:	4	Gaps:	29

Qy	36	PhaAspGlyThrThrsSerThrsPheSerSerLeuThrsSerSerAlaThrAspGly	55
Db	19	TACGATGGGAGACGTAACTGATCATCTTCCCTACTCTGTATAGAGATCCGAGTGG	78
Qy	56	ThrAsnTyValPheLeuAspSerValValIleGluAsnValProLeuThrglyGluThr	75
Db	79	ACTACTGTTTTTTCGACGAGAGATTAACATTAATAAAATCTTGCAATTCATATTCGACCT	138
Qy	76	GlnSerThrsCysPheLeuAsnAspAlaAlaAsglyAspLeuAsnPheLeuGly	95
Db	139	TTCGCTTTAAGTGTGTTGGGAAAC-----TTATTTAGGAGCTTTTACTGTTTAAAGGAGA	192
Qy	96	GlyPheSerPheThrsPheSerAsnIleAspAlaThrAlaSerGlyAlaAlaIleGly	115
Db	193	GGACACTCGTGTACTTTCGAGAAACATA---CGACCTTACAATATGGGACGCTCTAAGT	249
Qy	116	SerGluAlaAlaAsnLeuThrsValThrsLeuSerGlyPheSerAlaLeuSerPhe-----	133
Db	250	AATVAGCGTGTGATGAGACTGTTTACTTATGTAGAGGCTTTTAAAGAAATTAATCTTTTCCAAAT	309
Qy	134	-----LeuLeuSerPro	137
Db	310	TGCATTTCACTACTGCCGTACTGCCCTGCTGCACAGCTAAATAAGGTAGCCAGACTCCG	365
Qy	138	AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValGlyAsnLeuSerLeuLeu	157
Db	370	ACGACAACTCAACACCCGTATAGTACTTTTATTTCTAAACAGATCTTTGTCTACTC	429
Qy	158	AspAsnAspLeuValLeuIleGlnAspAsnPheSerThrglyAspGlyGlyAlaIleAsn	177
Db	430	AATTAATGAAAGATTCTCATTTATGTAATTTAGCTCTGAGATGGGGAGCTATAGAT	489
Qy	178	CysAlaGlySerLeuLeuIle-----	184
Db	490	---GCTAAAGGCTTAAGGCTTCAAGGAATTAAGCAAGCTTTGTCTTCCAAGAAATTAATCT	546
Qy	185	-----AlaAsn	187
Db	547	GCTCAAGCTGATGGGGAGCTTGTCAAGTAGTCACAGTTTCTCTGATGGCTAAACGAG	606
Qy	188	LeuSerLeuSerPheIleGlyAsnSerSerThrsThrglyGlyAlaIleHisThr---	206
Db	607	GCTCTATTGCTTTGTAGCGAATGTTGCAGAGATGAGAGGGAGGGGATTTGCTGCTTT	666
Qy	206	-----	206
Db	667	CAGATAGGCGACAGGAGATGTCATCATCTTCAACAGAAATCCAGTAGTAATTTT	726
Qy	206	-----	206
Db	727	TCCAAATACTACCGGTAGATTGTGATGGAAACGTAGCCCGAGTAGAGAGGATTTAC	786
Qy	207	-----LeuAsnLeuThrsLeuSerSerGlyGlyThrLeuPheGlnGlyAsnThrAla	224
Db	787	TCTACAGGGAAGTGTGCTTCTCTGAATATAGAAAAACCTTGTTTTCACAAATGTTGCT	846
Qy	225	-----ProThr-----	226
Db	847	TCTCTGTTTACATTGCTGCTAAGCAACAAACAAAGTAGACAGGCTTCTAATACGATTAAT	906
Qy	226	-----	226
Db	907	AATTACGAGATGAGAGAGCTATCTTCTGTAAAGATGTGCGCAGACAGATCCAAATAC	966
Qy	227	-----AlaAla	228

Db 967 TCTGATCAGTTCTTGTATGAGAGAGAGTAGTTTCTTATAGCAATGATGCT 1026
 Qy 229 G|Y|Y|----- 230
 Db 1027 GGGAAAGGGAGCTATTATGCAAAAGCTCTGGTTCATCTGGCCCTGACAA 1086
 Qy 231 -----G|Y|Y|A|I|E|A|I|E|A|A|S|P|S|E|Y|T|H|L|E|U| 242
 Db 1087 TTTTAAAGAAATATGCTATATGATGTGAGAGATTTATTTAGAGAAATCTGAGACTTC 1146
 Qy 243 SerIleSerGlyAspSerGlyAspIleIlePheGluGly----- 255
 Db 1147 ACTTATCTGCTGATATGAGATATATTTCTGATGGAATCTTAAAGACAGCAAA 1206
 Qy 256 ---AenThrIleGlyAlaThrGly---ThrValSerHisSerAlaIleAspLeuGlyThr 273
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 Qy 274 SerAlaIleValIleThrAlaLeuArgAlaIleGlnGlyHisIleThrIlePheTyrAspPro 293
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 Qy 294 IleThrVal---ThrGlySerThrSerValAlaAspAla-----LeuAsnIleAsn 309
 Db 1327 ATCGAATGCAAAAGCAAAATACAGCAGCAGCAGCTTCCAAACTTCTTAAATTAAC 1386
 Qy 310 SerProAspThrGlyAspAsnIleGlyTyrThrGlyThrIleValPheSerGlyGluYrs 329
 Db 1387 -----GATGGTAAAGATACACAGGCGGATATGTTTCT----- 1422
 Qy 330 LeuThrGluAlaGluAlaIleAspGluYrsAsnArgThrSerIleLeuLeuGlnAsnVal 349
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 Qy 350 AlaPheYrsAsnGlyThrValIleLeuYrsGlyAspValIleLeuSerAlaAsnGlyPhe 369
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 Qy 370 SerGlnAspAlaAsnSerIleLeuIleMetAspLeuGlyThrSerLeu----- 385
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 Qy 386 -----ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
 Db 1570 CCAACAACCAACAACAGCTCTGCGCTAATCAATGATCAAGCTTTCATCTGAT 1629
 Qy 399 IleAsnIleAspSerLeuArgAsnGlyYrsIle----- 410
 Db 1630 TTGTCTCTTCTTCTTTGATGCAACAAATGCAATGCAATCTCTCAATCTGAT 1689
 Qy 411 -----LysLeuSerAlaAlaIleThrAlaGlnLysAspIleArgIleAsp 424
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 Qy 425 ArgProValIleLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsnGlu 444
 Db 1750 GGGCTATCTTTTTCAGGATTTGATGATACAGCTTATGATGAG----- 1794
 Qy 445 AspHisSerTyrAsp-----GlyIleLeuGluLeuAspAla 456
 Db 1795 -----TATGATTTGGCTAGGATCTTAATCAAAAATCAATGATCTGTAATTAACGTTA 1845
 Qy 457 GlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSerPro--- 475
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 Qy 476 TyrGlyTyrGlnGlyYrsThrThrIleAsnThrPheSerThrAspAspLys----- 491
 Db 1906 TATGCTATCAAGAAAGCTGGAAGCTTGGAGATCTTAATACAGCAAAATTAATGCTCT 1965
 Qy 492 -----LysAlaThrValSerThrAlaYrsGlnSerPheAsnProThrAlaGlnGlu 508
 Db 1966 TATACTCTGAAGCTACA-----TGAAGTAAATCGGGATATATCTCTGGGCTGAGCGA 2019

Qy 509 GluAlaProLeuValProAsnLeuLeuThrGlySerPheIleAspValArgSerPheGln 528
 Db 2020 GTAGCTTCTTTGGTTCCAAAATATGTTATGAGGATCCATTTTATGATATGATCTGCCAT 2079
 Qy 529 AsnPheIleGluLeuGlyThrGluGlyValaProTyrGlyYrsArgPheThrValaIleGly 548
 Db 2080 TCAGCAATTCAGCAAGATGATGAGATGGGCTTATATGTCAGAGATTAATGGGTTTCTGGA 2139
 Qy 549 IleSerAsnValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSer 568
 Db 2140 GTTTCGAATTTCTTCTATCATGACCGCATCTTTAGCTCAGGATATCGGATATATTAAT 2199
 Qy 569 GlyIleValaValaIleValaIleSerThrArgMetProGlyGlyAspThrLeuSerLeuGly 588
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 Qy 629 LeuGlyGluGlyGlyLeuArgGluIleLeuLeuProTyrValSerLysThrLeuProCys 648
 Db 2371 TTCGAGATGGCGTTATCCG----- 2391
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 Db 2392 -----GCTAGTACGGGTTTGGAAATCAGCATATGAAACCTCATAT--- 2433
 Qy 669 ProProProProThrThrLeuSerThrAsp---HisThrSerThrGlyGlyTyrValIle 687
 Db 2434 -----ACATTTGCAAGAGAGAGAGCGATGTCCTGGATATATTAATCTGCTG 2478
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RESULT 9
 US-09-556-877-169
 ; Sequence 169, Application US/09556877
 ; Patent No. 6432916

GENERAL INFORMATION:
 APPLICANT: Probet, Peter
 APPLICANT: Bhakta, Ajay
 APPLICANT: Skeiky, Yasir
 APPLICANT: Piling, Steve
 APPLICANT: Malsomneuve, Jeff
 TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 FILE REFERENCE: 210121.469C5
 CURRENT APPLICATION NUMBER: US/09/556,877
 CURRENT FILING DATE: 2000-04-19
 NUMBER OF SEQ ID NOS: 305
 SOFTWARE: FastSeq for Windows Version 3.0/4.0
 SEQ ID NO 169
 LENGTH: 2643
 TYPE: DNA
 ORGANISM: Chlamydia
 US-09-556-877-169

Alignment Scores:
 Pred. No.: 1,766-66 Length: 2643
 Score: 711.50 Matches: 241
 Percent Similarity: 44.75% Conservative: 138
 Best Local Similarity: 28.45% Mismatches: 347
 Query Match: 16.57% Indels: 121
 DB: 4 Gaps: 31

US-09-830-446-27 (1-841) X US-09-556-877-169 (1-2643)

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 61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln----- 76
 358 ---CCTTCATATTATCA-----AAGATGTCAGTTATCTTCCCAATTAAT 405
 77 ---SerThrsCysPheLysAsn-----AspAlaAlaIleGlyAsp 89
 406 GGTGACATGAGTTCTGTCGAAATCATCTGAAAGCTCTGAGAGAGCATCTGCGAGT 465
 90 LeuAsnPhelGluGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrAla 109
 466 GCCTTCTTCTACAGACCAACTATCTTTTCAAGCTTTTCAAGAGAACTTTCTAAGGA 525
 110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLysSer---GlyPhe 128
 526 AATGGCGAGGCAATTCAGGCTCAA-----ACCTTCTCTTATCTAAGAAATGTC 573
 129 SerAlaLysSerPheLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
 574 TCCTCTATTTCTTCCGCGCTAATCTGCGAGT-----TTAATATGCG---GGCGCTAAT 624
 149 AsnValIleGlyAsnLysSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsn 168
 625 ---TGCTGATGATATCTTATTTGTTCAAGGAAATGAACCTCTCTTTTCACTGGAAC 661
 169 SerThrGlyAspGlyGlyAlaIleAsnGlyS-----AlaGly 180
 682 TCCGCACAGAAAGAGCGCTATTTGTTATCAGCATTAACAACCTCAGAAAAGGC 741
 181 SerLeuLysIleAlaAsnAsnLysSerLysSerPheIleGlyAsnSerSerThrAsp 200
 742 TCTCTCTCTTCTTCTGTAACCAAGAAACGCTATTGCAAGCAATCTGCTAAGAAAGA 801
 201 GlyGlyAlaAlaIleAsnThrLysAsnLysThrLysSerSerGlyGlyGluThrLysPheGln 220
 802 GGGGGGGCTATTATATGCAAGACATGATTTGCTTATACGCTCTGTTTCTTCAAT 861
 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
 862 AACCAACAGCGCTAAATA-----GGTGAAGCTATCCCATCCAGTCCGAGAGG 909

241 ThrLysSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile 258
 910 AGCTCTCATCTCTTCCAGGATGATGTTGTTCTTCCAGAAATATCCCAAGCAC 969
 259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
 970 TCCGACCAAGGCTAGTA---AGAAAGCATCTCTTATAGAAAGATCGATTCCTTCT 1026
 279 AlaLeuArgAlaAlaGlnIleAsnThrIleThrLysPheLysAspProIleThrValThrGly 298
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 299 SerThrSerValAlaAspAlaLeu-----AsnIleAsnSerPro--- 311
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 1366 ACTTCTTAAACCTCCCTCAT---TTGAAGTTAGCTACCTAAGTATCCCTTCAT 1422
 403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
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 462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyrosGlyTyrosIleLys 481
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 500 GlnSerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTrpGly 519
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 1819 TATCTATTGGAACGCGGAGATCTGCTGTTCTATTTATTTCTATGTCACAGACGCTCT 1878
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 578 ArgMetProGlyGlyAspThrLysSerLeuGlyPheAlaGlnLeuPheIleArgAspLys 597


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Db      1939 CACAGTTAGATGACCATCTTTCGCTTGCGCAGAGCAATTAATCTCGGGAATCGTCC 1998
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        1999 GATTCTCTATTACGCTACAGAAAGACCTCTATATAGCTACGTACAGACGGACATCC 2058
        618 AapAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyLeuArgGluIle 637
        2059 GCTACCTCTCTAATGAAATCTCTGCA----- 2085
        638 LeuLeuProTyrValSerIleThrLeuProCysSerPheTyrGlyGlyLeuSerTyrGly 657
        2086 -----CAGCAGATGCTACAT 2100
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        2146 GAAAGATTCAGATTCGCGATGAGCGTGGAGATCCGGAAGATGCGCATCGATCTCT 2205
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        717 AlaValTyrAlaGlyAsnSerPheValGlyLeuGlyAlaIleSerArgAspPheSer 736
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        2383 AAACAGCAACCTACTATTAATCTTCTAGAGAGCTTACCAAGACCTGAAACGTCATGTC 2442
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        795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
        2503 TTGGATTCAGAGCTCAATGTTCCGCTTACGAATCAAGAGCTTACAGACATTCAG 2562
        815 GluLeuPheGlyAsnPheGlyPheGluTyrArgGlySerSerArgSerTyrAsnValAsp 834
        2563 ACCGTGTA---AATGTGCTGTGTGTGCTGCGGCAAGCAATGTTACTCCCTGAT 2619
        835 AlaGlySerIleValIlePhe 841
        2620 CTGGGAGCACTTACAGGTTCT 2640
        RESULT 10
        US-09-620-169
        ; Sequence 169, Application US/09620412C
        ; Patent No. 6448234
        ; GENERAL INFORMATION:
        ; APPLICANT: Steven P. Fling
        ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
        ; FILE REFERENCE: 210121.469C7
        ; CURRENT APPLICATION NUMBER: US/09/620,412C
        ; CURRENT FILING DATE: 2000-07-20
        ; NUMBER OF SEQ ID NOS: 363
        ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
        ; SEQ ID NO 169
        ; LENGTH: 2643
        ; TYPE: DNA
        ; ORGANISM: Chlamydia
        ; US-09-620-412C-169

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Alignment Scores:
Pred. No.: 1,766-66 Length: 2643
Score: 711.50 Matches: 241
Percent Similarity: 44.75% Conservative: 138
Best Local Similarity: 28.45% Mismatches: 347
Query Match: 16.57% Indels: 121
DB: 4 Gaps: 31
US-09-830-446-27 (1-841) x US-09-620-412C-169 (1-2643)

QY      41 SerThrThrSerPheSerSerIleThrSerAlaThrAspGlyThrAsnTyrValPhe 60
        325 TCCTTCACAGATTGCTCTTCCAGAGAAAGCTCT----- 357
        61 LysAspSerValValIleGluAsnValProLysThrGlyIleThrGln----- 76
        358 ---CCTTCTATTATCATCA-----AAGATGATGATTAATCTTGGCGCATATAT 405
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        625 ---TCGCTAGTAATCTTATTATTTGTCAGGAAATGTAACCTCTCTTTTTCACCTGAAAC 681
        169 SerThrGlyAspGlyGlyAlaIleAsnCys-----AlaGly 180
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        802 GCGCGGCGCTATTATGCAAGCAATGATGATTCGTTTAAACGGTCTGTTTCTTCAAT 861
        221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAlaIleAlaIleAlaAspSerGly 240
        862 AACCAACAGCGCTAAATA-----GGTGAAGCTATGCGCATCCAGTCCGAGAGG 909
        241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile 258
        910 AGCTCTCTATCTTGGACGTGAAGATGCTGTTCTCCAGAAATACCTCCAGAGCACC 969
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        970 TCCGACCAAGGCTAGTA---AGAAACCCATCTCTTAAAGAAAGATCGCATTTCTTCT 1026
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QY 756 ---AlGIuGlnTyrThiSValValAlaMerTyrSerProAspValCysArgSerAsn 774
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 QY 775 ProLysCysThrThrThreuleuSerAsnGlnGlySerTrpYsrThrYsgLysSerAsn 794
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 DB 2620 CTGGGAGCACTTACAGGCTTC 2640
 RESULT 12
 US-09-556-877-181
 ; Sequence 181, Application US/09556877
 ; Patent No. 6432916
 ; GENERAL INFORMATION:
 ; APPLICANT: Probet, Peter
 ; APPLICANT: Bhatia, Ajay
 ; APPLICANT: Skeiky, Yasir
 ; APPLICANT: Piling, Steve
 ; APPLICANT: Malsomene, Jeff
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.469C5
 ; CURRENT APPLICATION NUMBER: US/09/556,877
 ; CURRENT FILING DATE: 2000-04-19
 ; NUMBER OF SEQ ID NOS: 305
 ; SOFTWARE: FastSeq for Windows Version 3.0/4.0
 ; SEQ ID NO 181
 ; LENGTH: 2601
 ; TYPE: DNA
 ; ORGANISM: Chlamydia
 US-09-556-877-181
 Alignment Scores:
 Pred. No.: 7,19e-65 Length: 2601
 Score: 696.50 Matches: 238
 Percent Similarity: 44.27% Conservative: 137
 Best Local Similarity: 28.10% Mismatches: 351
 Query Match: 16.22% Indels: 121
 DB: 4 Gaps: 31
 US-09-830-446-27 (1-841) x US-09-556-877-181 (1-2601)
 QY 41 SerThrThrSerPheSerSerLysTrpSerSerAlaThrAspGlyThrAsnTrpValPhe 60
 DB 283 TCTTTCACAGATGCTCTTCCAGAAAGCTCT----- 315
 QY 61 LysAspSerValValIleGluAsnValProLysTrpGlyGluThrGln----- 76
 DB 316 ---CCTTCAATATTATCA-----AAGATGTCAGTATCTTGGCAATAAT 363
 QY 77 ---SerThrSerCysPheLysAsn-----AspAlaAlaAlaGlyAsp 89
 DB 364 GGTGAGATAGATTTCTGTGCAATCATCTGAAAGCTCTGAGAGCCATCTCTGCGAT 423
 QY 90 LeuAsnPheLeuGlyGlyLysPheSerPheThrPheSerAsnIleAspAlaThrThrAla 109
 DB 424 GCCTTTCTTACAGCAACAATCTTTTACAGAGCTTTGAGAGAAATCTTTAAGGA 483
 QY 110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128
 DB 484 AATGGGAGGACCATTCAGGCTCA-----ACCTTCTTATCTAGAAATGTG 531

QY 129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
 DB 532 TCGCCATTTCTTTCGCGCATCGCCATCGCGGAT-----TTAAATGGC---GGCGCTATT 582
 QY 149 AsnValLysGlyAsnLeuSerLeuLeuAsnAspLysValLeuIleGlnAsnPhe 168
 DB 583 ---TGTGTAGTAATCTTATTGTTTTCAGGAATGTAAACCTCTCTTTTCACTGGAAC 639
 QY 169 SerThrGlyAspGlyGlyAlaIleAsnCys-----AlaGly 180
 DB 640 TCCGCCACAATAGAGGCGCTATTGTTGTATCAGAGATCTAAACCTCAGAAAAAGCG 699
 QY 181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
 DB 700 TCTCTCTCTTGTGCTTGTATCAABAACGATATTGCAAGCAATCTCTTAAAGAAAA 759
 QY 201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
 DB 760 GCGGGGCTATTATTCAGCAACATGTATTGCTTATACGCTCTGTTCTTCTCAT 819
 QY 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyAlaIleAlaIleAlaAspSerGly 240
 DB 820 AACACAGCGCTAAATA-----GGTGAAGCTATCGCATCCAGCCGAGG 867
 QY 241 ThrLeuSerLysSerGlyAspSerGlyAspIleIlePheGluLysAsnThr-----Ile 258
 DB 868 AGCTCTCTATCTTGTGAGTGAGGATCTGTCTGTTCCAAATPAACTCCACAGCACC 927
 QY 259 GlyAlaThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLysIleThr 278
 DB 928 TCCGACCAAGGCTAGTA---AGAAACGCATCTACTTACAGAAAGATCGATTCTTCT 984
 QY 279 AlaLeuArgAlaAlaGlnGlyHisThrThrIleYrPheYrAspProIleThrValThrGly 298
 DB 985 TCTTTGAAGCTCGCAACGA---GATATTCTTCTTGTGATCTTAT---GTACAGAA 1038
 QY 299 SerThrSerValAlaAspAlaLeu-----AsnIleAsnSerPro--- 311
 DB 1039 AGTACAGCAAGAAATCGGCTTCTTCCCTCTTTCGACCAAGCGTGACTCTCCAC 1098
 QY 312 -----AspThrGlyAspAsnLysGluTrpThrGlyThr 322
 DB 1099 CAGCCACCGCATCTCTTATGTTATTCAGACAACTGCAAAACCGT-----TCA 1146
 QY 323 IleValPheSerGlyGluLysLeuThrGluAlaGluAlaLysAspGluLysAsnArgThr 342
 DB 1147 GTGATTTCTCGAGGAACGCTTCTGAA---GAAGAAAAAACTCTGATTAACCTCACT 1203
 QY 343 SerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLysGlyAspVal 362
 DB 1204 TCCCAACTACAGACCTATTCGAACCTGAAATCCGACGCTTATTTAAAGATCGCGCT 1263
 QY 363 ValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGly 382
 DB 1264 GTCCTTCCGSCCTTCTCTCTCAGATCTCAAGCTCTCTCATATGGAAGCGGA 1323
 QY 383 ThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
 DB 1324 ACTTCTTAAAACTTCCCTTGTAT---TTGAAGTTAGTAGCTAGTATTCCTTCAT 1380
 QY 403 SerLeuArgAsnGlyLysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArg 422
 DB 1381 TCTTATGATCTGAATAAAGCTAACTATCCAGCC-----CTTATCTTCT 1428
 QY 423 IleAspArgProValValLeuAlaIleSerAspGluSerPheYrGlnAsn---GlyPhe 441
 DB 1429 ATCCAAAGATCTTCTCTCTAATCTGGAATGAGAAATTTTAAATAATAGAGCTT 1488
 QY 442 LeuAsnGluAspHisSerYrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
 DB 1489 CTCAGTAAAGACCAAAACAATATCTCTTACTTCTCCCTAAAGACCAATCTCATTTA 1548
 QY 462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProYrGlyTrpGlnGlyLys 481

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Db      1597 TGGACTTTTCTTGAAGATTCATGATGAGGCAATCTCTGATGATGAGGCGCT 1656
Qy      500 GlnSerPheAsnProThAlaGlnGlnAlaProLeuValProAsnLeuThrPgly 519
Db      1657 AAAAATACTGCTCATCCAGACAGCTCATCTTACCTCTTCCAGAACCTTTGGAAC 1716
Qy      520 SerPheIleAspValArgSerPheGlnAsnPhelIleGluLeuGlyThrGluValaPro 539
Db      1717 ACCTATCCGATATCAAGCTGAGCTGATGATGATTAATACAAACGCGAGAGAGAGCC 1776
Qy      540 TTTGluValArgPheThrValAlaGlyIleSerAsnVal-----LeuHisArgSerGly 557
Db      1777 TATCTATTGGAACCGTGGAGCTCTCTGTTCTTATTATGATGATGATGATGATGAT 1836
Qy      558 ArgGluAsnGlnArgLysPheArgHisValSerGlyValAlaValAlaValaSerThr 577
Db      1837 GCGAATACCTATGATATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1896
Qy      578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db      1897 CACAGTTAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1956
Qy      598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617
Db      1957 GATTCCTTATATCACTATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2016
Qy      618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyGlyLeuArgGluIle 637
Db      2017 GCTACTCTCTATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2043
Qy      638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657
Db      2044 -----CAGCAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2058
Qy      658 HisThrAspHisArgMetLysThrGlnSerLeuProProProProProProProPro 677
Db      2059 GAAATGATCCATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2103
Qy      678 Asp---HisThrSerTyrGlyGlyTyrValTyrAlaGlyLeuGlyThrArgValaLys 696
Db      2104 GAAAGATTCGATCTCTGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2163
Qy      697 ValGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheValaLysValGln 716
Db      2164 ATTTGA---TCAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2220
Qy      717 AlaValTyrAlaArgGlnAspSerPheValGluLeuGlyAlaIleSerArgAspPheSer 736
Db      2221 GGAATTTCAAGAACAGAGACGATTTTGAAGAGATTCGAGAGATTCGATGATGATGATGAT 2280
Qy      737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGlnLysArgPhe--- 755
Db      2281 GCGAGCTCTTCAAGAAATTTTCACTCTTATGAGAAATTAACATTTGAAAAAAATCCCAA 2340
Qy      756 ---AlaGlnGlnTyrTyrHisValAlaLysValaLysValaLysValaLysValaLys 774
Db      2341 AAAACAGAACATCATATATCTTCTAGAGAGCTATCAAGAGAGCTGAAAGAGATGATG 2400
Qy      775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerThrLysArgSerAsn 794
Db      2401 GAATCGGAGCTGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2460
Qy      795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
Db      2461 TTGATGATCAAGAGCTCAATGATTCGAGCTTACGAATCAAGAGCTTACAGAGATTCAG 2520
Qy      815 GlnLeuPheGlyAsnPheGlyPheGluTyrPargLysSerArgSerTyrAsnValaLys 834

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Db      2521 ACCTGTTA---AATGTCCTTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGAT 2577
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RESULT 13
US-09-620-412C-181
; Sequence 181, Application US/09620412C
; Patent No. 6448234
; GENERAL INFORMATION:
; APPLICANT: Steven P. Fling
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
; FILE REFERENCE: 210121.469C7
; CURRENT APPLICATION NUMBER: US/09/620,412C
; CURRENT FILING DATE: 2000-07-20
; NUMBER OF SEQ ID NOS: 363
; SOFTWARE: FastSeq for Windows Version 3.0/4.0
; SEQ ID NO 181
; LENGTH: 2601
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-620-412C-181

Alignment Scores:
Pred. No.: 7,19e-65 Length: 2601
Score: 696.50 Matches: 238
Percent Similarity: 44.27% Conservative: 137
Best Local Similarity: 28.10% Mismatches: 351
Query Match: 16.22% Indels: 121
DB: 4 Gaps: 31

US-09-830-446-27 (1-841) x US-09-620-412C-181 (1-2601)
Qy      41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db      283 TCCCTTACAGATGTCGTCCTTCCAGGAAGCTCT----- 315
Qy      61 LysAspSerValValIleGluAsnValProLysThrGlyGluThrGln----- 76
Db      316 ---CCTTCTATTATTCATCAA-----AAGATGTCGATTATCTTCCGCAATAT 363
Qy      77 ---SerThrSerCysPheLysAsn-----AspAlaAlaAlaGlyAsp 89
Db      364 GGTACATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 423
Qy      90 LeuAsnPheLeuGlyGlyGlyPheSerPheThrPheSerAsnIleAspAlaThrAla 109
Db      424 GCTTTTCTTACAGACAACTATCTTTTCAAGCTTTTGAAGAGATTTCTTAAAGCA 483
Qy      110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnLysThrValThrLeuSer---GlyPhe 128
Db      484 AATGCGGAGCATTCAGCTCAA-----ACCTTCTTTTATCTTAAAGATG 531
Qy      129 SerAlaLeuSerPheLeuLysSerProLysSerThrValThrAsnGlyLeuGlyAlaIle 148
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Qy      149 AsnValLysGlyAsnLeuSerLeuLeuAspAsnAspLysValLeuIleGlnAspAsn 168
Db      583 ---TGCCTAGTAATCTTATTTGTCAGAGAAATGAACCTCTCTTTTTCAGTGAAG 639
Qy      169 SerThrGlyAspGlyGlyAlaIleAsnCys-----AlaGly 180
Db      640 TCCGCGCAATATGAGAGGCTATTTGTTGATCAGCGATTAACACCTCAGAAAAAGGC 699
Qy      181 SerLeuLysIleAlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerThrArg 200
Db      700 TCTCTCTCTCTGCTTGTACCAAAACGCTATTGGAACAAATTCGCTTAAAGAAAAA 759
Qy      201 GlyAlaAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220

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Db 760 GCGGGGCTATTATGCGAAGCATGATATGCGTTATACGGCTCTGTTCTTCATT 819
 Qy 221 G1YAsnThrAlaProThrAlaAlaGlyGlyValAlaIleAlaIleAspSerGly 240
 Db 820 AACAAAGCCCTAAATAA-----GATGAGACTATCGCAATCCAGTCGAGG 867
 Qy 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile 258
 Db 868 AGCTCTCTATCTCTGAGGATGAGATGATCTGTTCTGATGCAATATCCCAACGAC 927
 Qy 259 G1YAlaThrGlyThrValIleSerIleAlaIleAspLeuGlyThrSerAlaValIleThr 278
 Db 928 TCCGACCAAGGCTTAGTA---AGAAAGCCATCTACTATGAGAAAGATGCAATCTTCT 984
 Qy 279 AlaLeuArgAlaAlaGlnGlyIleThrIleTyPheThrAspProIleThrValIleThrGly 298
 Db 985 TCTTATAGAGCTGCAACGGA---GATATCTTCTTATGATCTAT---GATCAAGAA 1038
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 Db 1147 GTGATTTCTCGAGCGAAGCGTCTTCTGA---GAAAGAAAACCTCTGATTAACCTCACT 1203
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 Qy 363 ValLeuSerAlaAsnGlyPheSerGlyAspAlaAsnSerIleLeuIleMetAspLeuGly 382
 Db 1264 GTCCTTCCSGGCTCTCTCTCAGAGATCTCAAGATCTCCCTCATATGAGAGCGGA 1323
 Qy 383 ThrSerIleValAlaAsnThrIleSerIleGluLeuThrAsnLeuGluIleAsnIleAsp 402
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 Qy 423 IleAspArgProValValIleuAlaIleSerAspGlySerPheTyroIleAsn---GlyPhe 441
 Db 1429 ATCCAAAGATCTTCTCTCTAATCTGAGATGAGATTTTATGAAAATGTAAGCTT 1488
 Qy 442 LeuAsnGluAspIleSerTyroAspGlyIleLeuGluLeuAspAlaGlyIleAspIleVal 461
 Db 1489 CTGAGTAAAGCAAAACATATTCCTCTCTAATCTCTCCCTAAGCAATCTCATTTA 1548
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 Qy 482 TyrThrIleAsnTyroSerThrAspAspIle-----LysAlaThrValIleSerThrAlaIle 499
 Db 1597 TGGACTTTTCTTGAAAAGATCTGATGAGGCAATCTCTGATGCTAATGTAAGCGCT 1656
 Qy 500 GlnSerPheAsnProThrAlaGlnGlnGluAlaProLeuValIleProAsnLeuLeuThrGly 519
 Db 1657 AAAAAGCTATGCTCTATCCAGAAAGCAATCAACATCTCTGCAACCTCTTGGAC 1716
 Qy 520 SerPheIleAspValIleArgSerPheGlnAsnPheIleGluLeuGlyThrGlnIleAlaPro 539
 Db 1717 ACTATTCGATATGCAAGCTGCTGACTCATATTAATCAACAGGCGACGAGAGACC 1776
 Qy 540 TyrGluIleAspThrProValAlaGlyIleSerAsnVal-----LeuIleAspSerGly 557
 Db 1777 TATCTATTGGAAGCGTGGATCTGCTTCTAATTTATTTATGTTTCAAGCAGCTCT 1836

Qy 558 ArgGluAsnGlnArgIlePheArgIleValIleSerGlyValAlaValAlaIleSerThr 577
 Db 1837 GGGAAACCTATCGATATATGCAATCGATACAGAGCTTGGCTTACTTATCCGATACGATCT 1896
 Qy 578 ArgMetProGlyIleAspThrIleuSerLeuGlyPheAlaGlnLeuPheAlaArgAspIle 597
 Db 1897 CACAGTTATGATGACCATCTCTTCTGCTGCTGAGAGCAATTAATCCGGAAATCGTCC 1956
 Qy 598 AspTyroPheMetAsnThrAsnPheAlaIleThrTyroAlaGlySerLeuArgLeuGlnIle 617
 Db 1957 GATTCCTTATATGCGTACAGAAAGCAACCTCTATATAGCTATGATACAGGCAATC 2016
 Qy 618 AspAlaSerIleuSerIleValIleSerIleLeuLeuGlyGluGlyIleuArgGluIle 637
 Db 2017 GCTACTCTCTATGAAAATCTCTGCA----- 2043
 Qy 638 LeuLeuProTyroValIleSerIleThrLeuProCysSerPheTyroGlyIleuSerTyroGly 657
 Db 2044 -----CAGGCACTCAAT 2058
 Qy 658 HisThrAspHisArgMetIleThrGluSerLeuProProProThrLeuSerThr 677
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 Qy 678 Asp---HisThrSerThrGlyIleTyroValIleTPAlaGlyGluLeuGlyThrArgValAla 696
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 Qy 697 ValGluAsnThrSerGlyArgIlePhePheGlnGlyIleThrProPheValIleValGln 716
 Db 2164 ATGTA---TCAATGCTTCCGAGCTGTCAGCTCTCTCTATTTCTTCTAATCGCA 2220
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 Qy 737 AspSerHisLeuTyroThrAsnAlaIleProLeuGlyIleLeuLeuGlyIleAspArgPhe--- 755
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 Qy 756 ---AlaGluGlnTyroTyroIleValAlaIleMetIleSerProAspValCysArgSerAsn 774
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 Qy 795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaIle 814
 Db 2461 TTGATTCAGAGGCTACATGTTCCGCTTACCAATCAAGAGCTTACACAGACTTCAG 2520
 Qy 815 GluLeuPheGlyAsnPheGlyPheGluTyroArgGlySerSerArgSerTyroAsnValAsp 834
 Db 2521 AGCGCTTA---AATGCTCTGTGCTGCTGCGGCAAAAGCATATGATCTCCCTGAT 2577
 Qy 835 AlaGlySerIleIleAspPhe 841
 Db 2578 CTGGGAGCACCTACAGTTTC 2598

RESULT 14

US-09-598-419-181
 ; Sequence 181, Application US/09598419
 ; Patent No. 6565856
 ; GENERAL INFORMATION:
 ; APPLICANT: Skeiky, Yasir A.W.
 ; APPLICANT: Scholler, John
 ; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR TREATMENT AND
 ; TITLE OF INVENTION: DIAGNOSIS OF CHLAMYDIAL INFECTION
 ; FILE REFERENCE: 210121.46906
 ; CURRENT APPLICATION NUMBER: US/09/598,419
 ; CURRENT FILING DATE: 2000-06-20

NUMBER OF SEQ ID NOS: 357
 SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
 SEQ ID NO: 181
 LENGTH: 2601
 TYPE: DNA
 ORGANISM: Chlamydia
 US-09-598-419-181

Alignment Scores:

Alignment No.:	7,196-65	Length:	2601
Score:	696.50	Matches:	238
Percent Similarity:	44.27%	Conservative:	137
Best Local Similarity:	28.10%	Mismatches:	351
Query Match:	16.22%	Indels:	121
DB:	4	Gaps:	31

US-09-830-446-27 (1-841) x US-09-598-419-181 (1-2601)

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QY 41 SerThrThrSerPheSerSerlySerThrSerSerAlaThrAspGlyThrAsnTyValPhe 60
DB 283 TCCTTCACAGATGCTCTTCACAGGAAGCTCT----- 315
QY 61 LysAspSerValValIleGluAsnValProlySerGlyGluThrGln----- 76
DB 316 ---CCTCTATTATTCATCA-----AGAAATGTCAGTTATCCTTGCGCAATAT 363
QY 77 ---SerThrSerCysPheLysAsn-----AspAlaAlaIleGlyAsp 89
DB 364 GGTACACATGATTTCTGTGAAATCATGCTGAAGCTCTGAGAGAGCCATCTCGGAT 423
QY 90 LeuAsnPheLeuGlyGlyIlePheSerPheThrPheSerAsnIleAspAlaThrAla 109
DB 424 GCCTTTCTCTACAGACACATATCTTTACAGCTTTGAGAGAAATCTTCTAAAGA 483
QY 110 SerGlyAlaAlaIleGlySerGluAlaAlaAsnlySerThrValThrLeuSer--GlyPhe 128
DB 484 AATGCGGAGCCATTCAGGCTCA-----ACCTCTCTTATCTAGAAATG 531
QY 129 SerAlaLeuSerPheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIle 148
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QY 149 AsnVallyGlyAsnLeuSerLeuLeuAspAsnAspIleValLeuIleGluAsnAsn 168
DB 583 ---TGCTGAGATATCTTATTGTTCAAGGAAATGAACCTCTCTTTTCACTGGAAC 639
QY 169 SerThrGlyAspGlyGlyAlaIleAsnGlyS-----AlaGly 180
DB 640 TCCGCCACCAATGAGGCGCTATTGTTATCAAGCATTAACACCTCAGAAAAAGGC 699
QY 181 SerLeuLysIleAlaAsnAsnlySerLeuSerPheIleGlyAsnSerSerThrArg 200
DB 700 TCTCTCTCTGCTGTGAACCAAAACGCTATTGTCAGACAAATCTCTTAAAGAAAA 759
QY 201 GlyGlyAlaIleHisThrLysAsnLeuThrLeuSerSerGlyGlyIleThrLeuPheGln 220
DB 760 GCGGGGCGATTATTAACCAACACATGATTCGCTTAACGCTCTGTTCTTCTTATT 819
QY 221 GlyAsnThrAlaProThrAlaAlaGlyGlyGlyAlaIleAlaIleAspSerGly 240
DB 820 AACCAACAGCGCTAAATA-----GGTGAAGCTATCGCCATCCAGTCGGAGGG 867
QY 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThr-----Ile 258
DB 868 AGCTCTCTATCTTCGACAGTGAAGATCTGTTCTTCAGAAATACCTCCAAACGACC 927
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QY 279 AlaLeuArgAlaAlaGlnGlyHisThrIleTyPheTyAspProIleThrValThrGly 298
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QY 312 -----AspThrGlyAspAsnlyGlyTyThrGlyThr 322
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QY 343 SerLysLeuGlnAsnValAlaPheLysAsnGlyThrValIleLeuLysGlyAspVal 362
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DB 1324 ACTCTTTAAAAAATCTCTTGAT---TTGAAGTAGSTACGTAATGATCCCTTAT 1380
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QY 423 IleAspArgProValIleLeuAlaIleSerAspGluSerPheTyGlnAsn--GlyPhe 441
DB 1429 ATCCAAAGATCTCTCTCTTAACCTGAGATGAGATTTTATGAAATGTAGAGCTT 1488
QY 442 LeuAsnGluAspHisSerTyAspGlyIleLeuGluLeuAspAlaGlyLysAspIleVal 461
DB 1489 CTCAGTAAAGACAAACAAATATCTCTCTTACTCTCTTAAAGACAAATCTCATTTA 1548
QY 462 IleSerAlaAspSerArgSerIleAspAlaValGlnSerProTyGlyTyGlnGlyLys 481
DB 1549 CATCTTCTGATGGAAC-----CTCTCTTCTCACTTGATATCAAGAGAT 1596
QY 482 TyrThrIleAsnTyPheThrAspAspLys-----LysAlaThrValSerTyrAlaLys 499
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QY 500 GlnSerPheAsnProThrAlaGluGlnAlaProLeuValProAsnLeuLeuTyrGly 519
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QY 520 SerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaPro 539
DB 1717 ACTTATTCGATATCAAGCTGTGCAATGATGATTAATCAACAGCCGACGAGAGACC 1776
QY 540 TyrGluLysArgPheTyrValAlaGlyIleSerAsnVal-----LeuHisArgSerGly 557
DB 1777 TATCATATTGGAACGTGGAGATCTGCTTTCTATTATTATCTATGATCACCAGAGCTCT 1836
QY 558 ArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAlaValAlaGlyLysSerThr 577
DB 1837 GGGAAACCTATCGATTAATTTGGCATATGAAAGCTTGACTACTATTCGATAGCTACT 1896
QY 578 ArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
DB 1897 CACAGTTTAGATGACATTTCTTCTGCTTGCTGACGACAAATTAATCTCGGAAATCTGCC 1956
QY 598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyAlaGlySerLeuArgLeuGlnHis 617
DB 1957 GATTCCTTATTAATGCTACAGAAACGACCTCTATATAGCTACTACAGACGCAATCTC 2016
QY 618 AspAlaSerLeuTySerValValSerIleLeuLeuGlyGlyGlyLysArgGluIle 637
DB 2017 GCTACCTCTTAATGAATAATCTGCA----- 2043
  
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QY 638 LeuLeuProTyValSerIyThrLeuProCySerPheTyGlyLeuSerTyGly 657
DB 2044 -----CAGGATGCTCAAT 2058
QY 658 HisThrAspHisArgPheClyThrGlySerLeuProProProThrLeuSerThr 677
DB 2059 GAAAGTATCCATAGCTAAACAAATAT-----CGCTCTCTCTAA 2103
QY 678 Asp---HisThrSerTrpGlyGlyValTrrAlaGlyGlyLeuGlyThrArgValAla 696
DB 2104 GAAAGATTGGATTCGGATAGCGTTGACATCCGAGAGAGTGGCGATGATCTCT 2163
QY 697 ValGluAsnThrSerGlyArgGlyPhePheGlnGlyTrpThrProPheValIysValGln 716
DB 2164 ATGTGA---TCAATGCTTCGAGCTGTTGAGCTCTCTCTATTTCTCTAACTGCA 2220
QY 717 AlaValTyrAlaArgIleAspSerPheValGlyLeuGlyValIleSerArgPheSer 736
DB 2221 GATTTTCAGGAACACAGGACGGTTTTCAGAGAGATTCGGAGATTCGGTCTTTCT 2280
QY 737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLeuSerGlyValArgPhe--- 755
DB 2281 GCCAGCTCTTTCAGAAATATTTCACTTCATAGAAATACATTGAAAAATCCCA 2340
QY 756 ---AlaGlnGlnTyrTrpHisValValAlaMetTyrSerProAspValCysArgSerAsn 774
DB 2341 AAAACGAAACCTACTTACTTCTTACAGAGCTTACCAAGCTCAAGAACTGATGTG 2400
QY 775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTrpThrIyGlySerAsn 794
DB 2401 GAATCCGAGACCTGATGTTACTCAAAAATGCCGTCTCGGATGCTCTATGCGAAC 2460
QY 795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAla 814
DB 2461 TTGGATTCACAGACCTTACGATTCGCTTACAAATCAAGAGCTTACACAGACTTCAG 2520
QY 815 GluLeuPheGlyAsnPheGlyPheGluTrpArgGlySerSerArgSerTyrAsnValAsp 834
DB 2521 AGCTGTGA---AATGTCTTGTGTGCTGCTGCGGCAAGCCATAGTACTCTCGAT 2577
QY 835 AlaGlySerIyIleLeuPhe 841
DB 2578 CTGGGAGCACCTTACAGGTTCT 2598

RESULT 15
US-09-556-877-171
; Sequence 171, Application US/09556877
; Patent No. 6432916
; GENERAL INFORMATION:
; APPLICANT: Probet, Peter
; APPLICANT: Bhatia, Ajay
; APPLICANT: Skeiky, Yasir
; APPLICANT: Fling, Steve
; APPLICANT: Malsomeuve, Jeff
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR TREATMENT AND
; FILE REFERENCE: 210121.469C5
; CURRENT APPLICATION NUMBER: US/09/556, 877
; NUMBER OF SEQ ID NOS: 305
; SOFTWARE: FASTSEQ for Windows Version 3.0/4.0
; SEQ ID NO 171
; LENGTH: 2895
; TYPE: DNA
; ORGANISM: Chlamydia
US-09-556-877-171

Alignment Scores:
Pred. No.: 1,71e-46 Length: 2895
Score: 527.50 Matches: 209
Percent Similarity: 37.54% Conservative: 121
Best Local Similarity: 23.78% Mismatches: 338
Query Match: 12.28% Indels: 211

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US-09-830-446-27 (1-841) x US-09-556-877-171 (1-2895)
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DB 457 GGAGCATTCATGCTCAAAATCTTTACATTAATCAATTAATCATGATGTGCGATTTTANG 516
QY 43 ThrSerPheSerSerIyThrSerAlaThrAspGlyThrAsn----- 57
DB 517 AAGACCTTTCTTANGTCCAGAGAGGACATTAGTACCGCTTAATCTTTGTTGAGC 576
QY 58 -----TyrValPheLysAspSerValIleGluAsnValProLysThr 72
DB 577 GAGATCAGCTTTGTTTCTTTATGACACACATCTGATTTCAACT----- 624
QY 73 GlyIuThrGlnSerThrSerCysPheLysAsnAspAlaAlaGlyAspLeuAsn 92
DB 625 -----AATACAGACAGAAAGTGGCGCTATCTAT 654
QY 93 LeuGlyGlyIyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAla 112
DB 655 GCTGGAACGAGCAATTTCTTTGAGAGTAAATACCTGCAATCTTCTTCAATCAATACGCC 714
QY 113 AlaIleGlySerGlyAlaAlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSer 132
DB 715 TGTTCGACAGAGAGCG----- 732
QY 133 PheLeuLysSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGly 152
DB 733 ---ATCTTCTCCCTATCTGTTCTTCAACAGAAAT-----CGTGT 771
QY 153 AsnLeuSerLeuLeuAsnAsnAsp-----LysValLeuIleGlnAsnAsnPheSerThr 170
DB 772 AACATGTTTCTATATATACATGCTGCTTAAATATGAGAAACAGCTTCTTCAAGAGCT 831
QY 171 GlyAspGlyGlyAlaIleAsnLysAlaGlySerLeuLysIleAlaAsnAsnLysSer--- 189
DB 832 TCTGATGAGAGCAATTAAGTAATCTCGCTGATGATTTACAGGCAATCTCGTAGG 891
QY 190 LeuSerPheIleGlyAsnSerSerThrArgGlyGlyAlaIleHisThrLysAsnLeu 209
DB 892 ATCTTTTATGACAAATATCACAAAATAATATGCGAGATTTATACGCTCTGTAGTT 951
QY 210 ThrLeuSerSerGlyGlyGluThrLeuPheGlnGlyAsnThrAlaProThrAlaAlaGly 229
DB 952 ACCCTAGTGATTAATGCGCTTACTTATTAATTAAT-----ATCGCAATTAAT 1002
QY 230 LysGlyGlyAlaIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGly 249
DB 1003 AAGGGGGGCGCTATATATAGACGAGACCACTACTCCAAAATTTCTGCCGCGCCAT 1062
QY 250 AspIleIlePheGluGlyAsnThrIle-----GlyAlaThrGlyThrValSer 265
DB 1063 GCATATATTTTAATGAATAATTTGACTAATGTAATCAATGCAATGATACAGTAGG 1122
QY 266 -----HisSerAlaIleAspLeuGlyThrSerAlaLysIleThrAla 279
DB 1123 TCAGCTAATCTCTTACAGAAATGCAATTAACAGTACGCACTCTGCTGTAATTTCA 1182
QY 280 LeuArgAlaAlaGlnGlyHisThrIleTyrPheTyrAspProIleThrValThrLysSer 299
DB 1183 TTGGAGCGAGAGTACCAAAATTTATTTTATGATCTTATTAAGTTAGC---AAT 1239
QY 300 ThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLysGlyTyr 319
DB 1240 GCAAGGCTCTGCTGTGCTTCAAT-----AAGAAAGCTGATCA 1278
QY 320 ThrGlyThrIleValPheSerGlyGlyLysLeuThrGluAlaGlyAlaLysAspGlyLys 339
DB 1279 ACAGGCTCTGTAGTATTTTACAGAGCTACTGTTATTTCTGCAAGATTT---CATCAAGC 1335
QY 340 AsnArgThrSerLysLeuLeuGlnAsnValAlaPheLysAsnGlyThrValValLeuLys 359

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Db      1336  AATTATCAAAACAAAACCTGCACCCCTTACTCTCAGTAAGGTTTCTATGATCCAA 1395
      360  GlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerIleuIleMet 379
      1396  GATATGCTGACCTTACAGTGAATGATTCACACAACTGGGGGT-----GTGTT 1446
      380  AspleuGlyThrSerLeuVal-----AlaAsn 388
      1447  TCTCTGGGAATGAGACAGTTCTGAGTGTCTATAAAATGATGACAGAGATTCTGCTAGC 1506
      389  ThrGluSerIleGluLeuThrAsnLeuGlnIleAsnIleAspSer---LeuArgAsnGly 407
      1507  AATGCTCTATTAACACTGAAGCATTTGGAATTTCTTCTCATCTGTAAGAAAGTGT 1566
      408  LysIleIleLeuLeu-----SerAlaIleThrAlaGlnIleAspIleArgIleAsp 424
      1567  GCTGAGATTCCTTATTTGTGGGTAGAGCTCAAAATTAACAGCAATTAATCAACAGAT 1626
      425  ArgProValValLeuAlaIleSerAsp-----Glu 434
      1627  ACTGCAGCTACCTTCTTATGATGTAATAAACTCTCAGCATGATGACTAGAGGAAC 1686
      435  SerPheTyrglnAsnGlyPheLeuAsnGlnAspHisSerTyrglyIleLeuGlnLeu 454
      1687  TCTCTTATGATCAACAGATCTGACCCATGCTCTGTCATCAACAGCTATGCTATTA 1746
      455  AspAlaGlyLysAspIleValIleSerAlaAspSerArgSerIleAspAlaValGlnSer 474
      1747  TCTGAAGCTAGGATTAACAGCTACATCAAGAAATTAATGATTTTCGGAGCTAAATGTC 1806
      475  Pro---TyrglyTyrglnGlyLysSerThrIleAsnIlePheSer----- 487
      1807  CCTCATTTATGATGCAAGGACTTTTGACTTGGGGCTGGGCAAAAACCAAGATCCAGA 1866
      488  -----ThrAspAspIleValIleThr----- 494
      1867  CCAGCATCTTCAGCAACAATCACTGATCCACAAAAGCCAAATGATTTCTATGAACCTTA 1926
      495  ---ValSerThrAlaIleGlnSerPheAsnProThrAlaGlnGlnAlaProLeuVal 513
      1927  CTACTTAACATGCTTCCTCCGGGGTATGTTCTTACGCCAAAACACAGAGTCCCTCATTA 1986
      514  ProAsnLeuLeuTyrglySer---PheIleAspValArgSerPheGlnAsnPheIleGln 532
      1987  GCTAACACCTTATGCGGGAAATGCTGCTGCAACAGAAAGCTTAATAAATGTCAGAG 2046
      533  LeuGlyThrGlnGlyAlaProTyrglyLysArgPheTrp-----ValAlaGlyIle 549
      2047  CTGACACCTAGTGTGATCTCT-----TTCTGGGGAATTACAGAGAGAGACTTA 2094
      550  SerAsnValLeuHisArgSerGlyArgGlnAsnGlnArgLysPheArgHisValSerGly 569
      2095  GGCATGATGCTTTACCAAGATCTCGAAGAAATCATCTCGATTCATATGGCTCTTCC 2154
      570  GlyAlaValValGlyAlaSerThrArgMetProGlyGlyAsp-----ThrLeuSerLeu 587
      2155  GGATTACTCGCGGG-----ATGATAGCAGGGGAGACACACACCTTCTCATTTG 2202
      588  GlyPheAlaGlnLeuPheAlaArgAspLysAspTyrgPheMetAsnThrAsnPheAlaLys 607
      2203  AAATTCAGTCAGACCTCAACCAAA-----CTCAATGAGCGTTACGCCAAA 2247
      608  ThrTyralaGlySerLeuArgLeuGlnHisAspAlaSerLeuTyrgSerValValSerIle 627
      2248  AACAACGATATCTTCT-----AAAATTACTCATGCCAAGAGAAATGCTCTTC 2295
      628  LeuLeuGlyGlnGlyGlyLeuArgGlnIleLeuLeuProTyrgValSerIleThrLeuPro 647
      2296  TCATTGCAAGAAAGGTTTCTTGCTGACTAAATTAAGTT----- 2331
      648  CysSerPheTyrglyGlnLeuSerTyrgly---HisThrAspHisArgMetLysThrGln 666

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Db      2332  -----GGGCTTTACAGCTANGAGACCATTACTGTCAACCATTTCTATACTCA 2379
      667  SerLeuProProProProThrLeuSerThrAspHisThrSerTyrglyTyrgVal 686
      2380  GGA----- 2382
      687  TrpAlaGlyLeuGlyThrArgValAlaValGlnAsnThrSerGlyArgGlyPhePhe 706
      2383  -----GAAATCTAACATCTCAAGGACGTTCC 2409
      707  GlnGlnTyrgThr----- 710
      2410  CGCAGTCAAACGATGGAGAGGTGCTGTTTGTATCTCCCTATGAACCTTTGGATCA 2469
      711  -----ProPheValIleValGlnAlaValTyrgAlaArgGlnAspSer 724
      2470  ACGCATATACAGACGCTCCCTTTTATAGTCTCTTGATTTATTTACGCTGTCTCAC 2529
      725  PheValGlnLeuGlyAlaIleSerArgAspPheSer---AspSerHisLeuTyrgAsnLeu 743
      2530  TTTACTGAGGTGGAGGCTTATCCCGGAAGCTTTTCTACAAAGACTCTTGATCATATGTC 2589
      744  AlaIleProLeuGlyIleLys-----LeuGlnLysArgPheAlaGlnGlnTyrg 760
      2590  CTAGTCCCTATTTGAGATTAAGGTAGCTTTATGATGATGCTACCAACAGACTCAAGCCTGG 2649
      761  HisValValAlaMetTyrgSerProAspValCysArgSerAsnProLysCysThrThr 780
      2650  ACTGTAAATGGCATACCAACCCGTTCTGTATAGACAGAAACCGAGGATGCGACCCAG 2709
      781  LeuLeuSerAsnGlnGlySerTyrgLysThrLysGlySerAsnLeuAlaArgGlnAla 799
      2710  CTCCTAAGCAGTAAGGATTTGTTGTGTAGTGAAGCCCTCATGCGCGATGCGC 2766

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Search completed: January 29, 2004, 17:03:03
Job time : 1583 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 ; Search time 722 Seconds
(without alignments)
4245.252 Million cell updates/sec

Title: US-09-830-446-27
Perfect score: 4235
Sequence: 1 MKIPRFLISLVPTLSMSN.....FEWGRSSRSYVDAGSKIKF 841

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2434939 seqs, 1822278265 residues
Total number of hits satisfying chosen parameters: 4869878

Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters: -MODE=frame+ p2n model -DRV=xlib
-O=/cgn2_1/USPTC_spool/US0983044/runat_29012004_102103_19252/app_query.fasta_1.1031
-DB=Published Applications NA -QMT=faetap -SUFFIX=p2n.tmpb -MINMATCH=0.1
-LOOPEL=0 -LOOPEXT=0 -UNITS=bits -START=1 -END=1 -MATRIX=blosum62
-TRANS=human40.cdi -LIST=45 -DOCLIGN=200 -THR SCORE=pcp -THR MAX=100
-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pcp -NORM=ext -HAPSTER=500 -MINLEN=0
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-NCPU=6 -ICPU=3 -NO MAP -LANG=ENGLISH -NEG_SCORES=0 -WAIT -DSBLOC=100
-LONGLOG -DRV_TIMEOUT=120 -WANT_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5
-FGAPOP=6 -FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : Published Applications NA:
1: /cgn2_6/ptodata/1/pubpna/US07_PUBCOMB.seq:
2: /cgn2_6/ptodata/1/pubpna/PCT_NEW_PUB.seq:
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9: /cgn2_6/ptodata/1/pubpna/US09_PUBCOMB.seq:
10: /cgn2_6/ptodata/1/pubpna/US09C_PUBCOMB.seq:
11: /cgn2_6/ptodata/1/pubpna/US09B_PUBCOMB.seq:
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14: /cgn2_6/ptodata/1/pubpna/US10B_PUBCOMB.seq:
15: /cgn2_6/ptodata/1/pubpna/US10_NEW_PUB.seq:
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18: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq:

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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1	4295	100.0	2526	12	US-10-312-273-140	Sequence 140, App
2	4255	99.1	1230025	12	US-10-289-762-1	Sequence 1, Appl1
3	1580.5	36.8	3000	13	US-09-428-122-1	Sequence 1, Appl1
4	1497	34.9	2520	13	US-09-738-269-22	Sequence 22, Appl1
5	1497	34.9	2520	14	US-10-023-437-22	Sequence 22, Appl1
6	1435.5	33.4	2787	12	US-10-312-273-116	Sequence 116, App
7	1415.5	33.0	2793	12	US-10-312-273-96	Sequence 96, Appl1
8	1407.5	32.8	2787	12	US-10-312-273-56	Sequence 56, Appl1
9	1379.5	32.1	2787	12	US-10-312-273-44	Sequence 34, Appl1
c	1365	31.8	1230025	12	US-10-289-762-1	Sequence 1, Appl1
10	1357.5	31.6	2241	12	US-10-312-273-20	Sequence 20, Appl1
11	1335.5	31.1	2811	12	US-10-312-273-154	Sequence 154, App
12	1335.5	31.1	3050	9	US-09-452-380-1	Sequence 1, Appl1
13	1335.5	31.1	3051	13	US-10-324-129-1	Sequence 1, Appl1
14	1335.5	31.1	3050	13	US-10-312-273-4	Sequence 4, Appl1
15	1286.5	30.0	2781	13	US-09-738-269-56	Sequence 56, Appl1
16	1286.5	30.0	2781	14	US-10-023-437-56	Sequence 56, Appl1
17	1279.5	29.8	2808	9	US-09-452-380-2	Sequence 2, Appl1
18	1279.5	29.8	2808	13	US-10-324-129-2	Sequence 2, Appl1
19	1089	25.4	2922	12	US-10-312-273-4	Sequence 4, Appl1
20	1016	23.7	2769	12	US-10-312-273-42	Sequence 42, Appl1
21	1011	23.5	2950	9	US-09-886-468-6	Sequence 6, Appl1
22	1002	23.3	4224	9	US-09-841-132-486	Sequence 486, App
23	1002	23.3	4224	12	US-10-312-273-32	Sequence 32, Appl1
24	936	21.9	3021	9	US-09-841-132-182	Sequence 182, App
25	936	21.8	2949	9	US-09-841-132-170	Sequence 170, App
26	828.5	19.3	2040	13	US-09-738-269-52	Sequence 52, Appl1
27	828.5	19.3	2040	14	US-10-023-437-52	Sequence 52, Appl1
28	711.5	16.6	2643	9	US-09-841-132-169	Sequence 169, App
29	696.5	16.2	2601	9	US-09-841-132-181	Sequence 181, App
30	648	15.1	1065	12	US-10-312-273-16	Sequence 16, App
31	559	13.0	1485	12	US-10-312-273-134	Sequence 134, App
32	557	13.0	1745	9	US-09-886-468-10	Sequence 10, Appl1
33	555	12.9	1545	12	US-10-312-273-52	Sequence 52, Appl1
34	548.5	12.8	1188	12	US-10-312-273-22	Sequence 22, Appl1
35	536.5	12.5	5172	9	US-09-841-132-374	Sequence 374, App
36	536.5	12.5	5172	9	US-09-841-132-375	Sequence 375, App
37	536.5	12.5	5172	12	US-10-312-273-120	Sequence 120, App
38	527.5	12.3	2895	9	US-09-841-132-171	Sequence 171, App
39	527.5	12.3	2934	9	US-09-841-132-183	Sequence 183, App
40	509.5	11.9	3050	10	US-09-779-081-1	Sequence 1, Appl1
41	509.5	11.9	4830	12	US-10-312-273-84	Sequence 84, Appl1
42	509.5	11.9	4830	13	US-09-841-260-59	Sequence 59, Appl1
43	509.5	11.9	4830	14	US-10-007-693-59	Sequence 59, Appl1
44	506	11.8	5265	9	US-09-841-132-174	Sequence 174, App
45	502	11.7	5253	9	US-09-841-132-421	Sequence 421, App

ALIGNMENTS

RESULT 1
US-10-312-273-140
Sequence 140, Application US/10312273
Publication No. US2004000567A1
GENERAL INFORMATION:
APPLICANT: CHIRON SPA
TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
FILE REFERENCE: P025035MO
CURRENT APPLICATION NUMBER: US/10/312.273
CURRENT FILING DATE: 2002-12-20
PRIOR APPLICATION NUMBER: 0016363.4
PRIOR FILING DATE: 2000-07-03
PRIOR APPLICATION NUMBER: 0017047.2
PRIOR FILING DATE: 2000-07-11
PRIOR APPLICATION NUMBER: 0017983.8
PRIOR FILING DATE: 2000-07-21
PRIOR APPLICATION NUMBER: 0019368.0
PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: 0020440.4
PRIOR FILING DATE: 2000-08-18
PRIOR APPLICATION NUMBER: 0022583.9
PRIOR FILING DATE: 2000-09-14
PRIOR APPLICATION NUMBER: 0027549.5
PRIOR FILING DATE: 2000-11-10

; PRIOR APPLICATION NUMBER: 0031706.5
 ; PRIOR FILING DATE: 2000-12-22
 ; NUMBER OF SEQ ID NOS: 664
 ; SOFTWARE: Seqwinn9, version 1.02
 ; SEQ ID NO 140
 ; LENGTH: 2526
 ; TYPE: DNA
 ; ORGANISM: Chlamydia pneumoniae
 US-10-312-273-140

Alignment Scores:
 Pred. No.: 0 Length: 2526
 Score: 4295.00 Matches: 841
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 Gaps: 0

US-09-830-446-27 (1-841) x US-10-312-273-140 (1-2526)

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 21 LeuleuGlyAlaIleThrThrgluGluLeuSerAlaSeranSerPheApoIYThrThr 40
 61 TTATTAGAGAGCTGCTACACCAAGATTTATCGCTTAGCAATAGCTTTCATGGAATCA 120
 41 SerThrThrSerPheSerSerleYThrSerSerAlaThrApoIYThrApoIYThrValPhe 60
 121 TCACACACACAGCTTTCTTCATGAACATCATCGGCTACAGATGACCACTATATGTTTT 180
 61 LysApoSerValValIleGluLeuValIleProYThrThrgluIleThrlleuSerThrSerCys 80
 181 AAGAGATTCGTAGTATAGAAAATGATACCCAAACAGGGGAACTCAGCTACATGATGTGT 240
 81 PheLYsApoSerAlaAlaIleGlyApoLeuApoPheleuGlyGlyYpPheSerPheThr 100
 241 TTTAAATAATGACGCTGACCTGACATCTAAATTTCTTAGAGGGGATTTCTTTTACA 300
 101 PheSerApoIleApoAlaThrThrlaSerGlyAlaIleGlySerGluAlaIleApo 120
 301 TTTAGCAATATGATGATGACCAACAGGCTTCGAGCTGATAGGAAGTACACACTAT 360
 121 LysThrValThrlleuSerGlyPheSerAlaLeuSerPheleuLysSerProAlaSerThr 140
 361 AAGACAGTCACGTTATACAGATTTTCGCACTTTCTTTCTTAAATCCCCACCAAGTACA 420
 141 ValThrApoGlyLeuGlyAlaIleApoValIleGlyApoLeuSerleuLeuApoApo 160
 421 GTGACCTATGAGTTGGAGCTATCATATGTTAAAGGAATTTAAAGCTTATGATATATGAT 480
 161 LysValleuIleGlyApoApoPheSerThrglyApoGlyGlyAlaIleApoCysAlaGly 180
 481 AAGATATGATTCAGGACCAATTTCTCAACAGAGAGTGGGACATTAATGTCAGGCG 540
 181 SerleuLysIleAlaApoApoLysSerleuSerPheIleGlyApoSerSerThrArg 200
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 201 GlyGlyAlaIleIleThrlYsApoLeuThrlleuSerSerGlyGlyGluThrlleuPheGln 220
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Best Local Similarity:	99.76%	Mismatches:	1
Query Match:	99.07%	Indels:	2
DB:	12	Gaps:	0

US-09-830-446-27 (1-841) x US-10-289-762-1 (1-1230025)

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QY 21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAanSerPheAspGlyThrThr 40
DB 29010 TTATTAGGAGCTGCTACTACCCAGAGATTATCGCTAGCAATAGCTTCATGAACTACA 29069
QY 41 SerThrThrSerPheSerSerIleThrSerSerAlaThrAspGlyThrAanTyrValPhe 60
DB 29070 TCACACACAGCTTTTCTAGTAAACATCATCGCTACAGATGGACCAATTATGTTTTT 29129
QY 61 LysAspSerValValIleGluAanValProLysThrGlyIleThrGlnSerThrSerCys 80
DB 29130 AAAAGATTCTGTAGTATAGAAAATGATACCAAAACAGGGGAACTCAGTCTACTAGTTGT 29189
QY 81 PheLysAanAspAlaAlaIleGlyAspLeuAanPheLeuGlyGlyIlePheSerPheThr 100
DB 29190 TTTAAATAAGACGCTGACGCTGAGATCTAAATTTCTTAGAGGGGGATTTTCTTTCACA 29249
QY 101 PheSerAanIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAan 120
DB 29250 TTTAGCAATATCGATCGAACCAACGCTTGTGAGCTGCTATGGAAGTAAACAGCTAAT 29309
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DB 29310 AAGACAGTCACGTTATCAGATTTTCGGCACTTCTTTCTTAAATCCCAAGCAAGTACA 29369
QY 141 ValThrAanGlyLeuGlyAlaIleAanValLysGlyAanLeuSerLeuLeuAanAspAan 160
DB 29370 GTGACTAATGATGGAGCTATCAATGTTAAAGGAATTTAAGCTTATGATATGAT 29429
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Qy 201 GlyGlyAla11eH1eThrLysAsnLeuThrLeuSerSerGlyGlyGluThrLeuPheGln 220
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Qy 221 GlyAsnThrAlaProThrAlaAlaGlyLysGlyGlyAla11eAla11eAlaAspSerGly 240
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Qy 241 ThrLeuSer11eSerGlyAspSerGlyAsp11e11ePheGlyGluGlyAsnThr11eGlyAla 260
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US-09-428-122-1
; Sequence 1, Application US/09428122
; Publication NO. US20030170259A1
; GENERAL INFORMATION:
; APPLICANT: Connaught Laboratories Limited
; APPLICANT: Murdin et al.

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TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
 TITLE OF INVENTION: US98-007-019
 FILE REFERENCE: 19721-007-019
 CURRENT APPLICATION NUMBER: US/09/428,122
 CURRENT FILING DATE: 1999-10-27
 EARLIER APPLICATION NUMBER: 60/106,046
 EARLIER FILING DATE: 1998-10-28
 EARLIER APPLICATION NUMBER: 60/132,271
 EARLIER FILING DATE: 1999-05-03
 NUMBER OF SEQ ID NOS: 4
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 1
 LENGTH: 3000
 TYPE: DNA
 ORGANISM: Chlamydia pneumoniae
 FEATURES:
 NAME/KEY: CDS
 LOCATION: (101)..(2884)
 US-09-428-122-1

Alignment Scores:
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US-09-830-446-27 (1-841) x US-09-428-122-1 (1-3000)

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DB 1961 ATTAGCTCTCTCATTTATCTTATAGAGACTCGAAGAGGGTGCAGGAGACCTGCT 2020
QY 544 PheTPValaLagLyl1eSerAenValLeuH1eArgSerGlyArgGlnAenGlnArgLys 563
DB 2021 TTTGGTGCGGAGATATCTAATCTCTCCATNAAGATAGTACAAAACAGACCCGGG 2080
QY 564 PheArgH1eValSerGlyLysValValValGlyAlaSerThraArgSerProGlyLysAap 583
DB 2081 TTTCCGCAATTTGAGTGGCGGTTATGTCAATAGGAGAACTCATGCTTTCAGATAG 2140
QY 584 ThrLeuSerLeuGlyPheAlaGlnPheAlaArgAspLysAspPhePheLeuAenThr 603
DB 2141 ATCTTAGCGCTGCAATTTGTCTGAGCTCTTGGAGAGATAGAGACTATTGTGAGTAA 2200
QY 604 AenPheAlaLysThrThraLagLysLeuArgLeuGlnH1eAspAlaSerLeuTyrSer 623
DB 2201 AATCAAGATACAGTCTCAAGAGAGACTCTCTATACAGACAGACAACTATATCTCT 2260
QY 624 ValValSerLeuLeuGlyLysGlyLysLeuArgGlnLeuLeuProGlyValSer 643
DB 2261 CTTCCTTGC-----AACTACGCGCTGTGTGCTTGTCTTATGTTCT 2302
QY 644 LysThrLeuProCysSerPheTyrGlyLysLeuSerTyrGlyH1eThraAspH1eAagMet 663
DB 2303 ACAGAGATTCCTGTTCTCTTTCAGAGAACTTACGTAACCCATACGATTAACATTCG 2362
QY 664 LysThrGlnSerLeuProProProProThrLeuSerThraAspH1eThraSerTPGly 683
DB 2363 AAAACCAATAT-----ACAGCATATCCATCTTAAAGAAAGCTGGGG 2407
QY 684 GlyTyrValTPAlaGlyLeuGlyLysThraArg-----ValAlaValGlnAenThrSer 701
DB 2408 AATGATAGTTCGCTTATAGATTCGATGAGAGAGCTCCATTTGCTTATAGTAAAGTGT 2467
QY 702 GlyArgGlyPhePheGlnGlnLysThrProPheValLysValGlnAlaValTPAlaAag 721
DB 2468 -----CTATTAGAGAGATGATGCCCTTCATGAAATGCAATTTGTCTATGCAAT 2518
QY 722 GlnAerSerPheValGlyLeuGlyAlaL1eSerArgAspPheSerAerPheH1eLeuTyr 741
DB 2519 CAGGAAGCTTTAAAGACAGGAGACAGAGCTCGTGAATTTGAAAGTGAAGCTCTTGTG 2578
QY 742 AenLeuAlaL1eProLeuGlyLysLeuGlyLysArg-----PheAlaGlnGlnTyr 759
DB 2579 AATCTTCCTTACCTTATCGGAGATCCGATTTGATTAAGAAATGACAGCTGCCAAGTGA 2638
QY 760 TyrH1eValValAlaMetTyrSerProAerPvalCysArgSerAerProLysCysThrThr 779
DB 2639 TACAACTTACTCTTGTTATCTGATCTGTGATCTGTTCGATGAACCCCACTGTATAGACA 2698
QY 780 ThrLeuLeuSerAenGlnGlySerTPLyThrLysGlySerAenLeuAlaArgGlnAla 799
DB 2699 AACCTCGCAATTAAGCGGATCTTGGAAAACCTTGGTACGAATTTGGCAAGACAGCT 2758
QY 800 GlyLysValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaLagLysLeuPheGlyAen 819
DB 2759 TTAGTCTCTCGAGAGAGACATTTTGTCTTATACCAATTTGAGAGCTTTAGCCAA 2818
QY 820 PheGlyPheGlnLysThraGlyLysSerArgSerTyrAenValAspAlaGlySerLysLe 839
DB 2819 TTTCTTTGAATGCGTGGTCTATCTCGCAATTAACATGTAGACTTAGAGAGCAAAATAC 2878
QY 840 LysPhe 841

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DB 2879 CAATTC 2884
RESULT 4
US-09-738-269-22
/ Sequence 22, Application US/09738269
/ Publication No. US20030185848A1
/ GENERAL INFORMATION:
/ APPLICANT: JOHNSTON, STEPHEN A.
/ APPLICANT: STENKE-HALE, KATHERINE
/ APPLICANT: SYKES, KATHRYN F.
/ APPLICANT: KALTENBOECK, BERNHARD
/ TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
/ TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
/ FILE REFERENCE: US/09-738-269
/ CURRENT APPLICATION NUMBER: US/09/738,269
/ NUMBER OF SEQ ID NOS: 61
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 22
/ LENGTH: 2520
/ TYPE: DNA
/ ORGANISM: Chlamydia psittaci
US-09-738-269-22
Alignment Scores:
Pred. No.: 3,15e-143 Length: 2520
Score: 1497.00 Matches: 357
Percent Similarity: 56.21% Conservative: 132
Best Local Similarity: 41.03% Mismatches: 321
Query Match: 34.85% Indels: 60
DB: 13 Gaps: 25
US-09-830-446-27 (1-841) x US-09-738-269-22 (1-2520)
QY 1 MetLysL1eProLeuArgPheLeuLeuL1eSerLeuValProThrLeuSerMetSerAen 20
DB 1 ATGAACATCCAGTCTACTGCTTATATCC-----TCAGGCTATTTGCCGAT 54
QY 21 LeuLeuGlyAlaL1eThrThrGlnLys-----LeuSerAlaSerAenSerPheAspGly 38
DB 55 TCTTGAAGCTTGTCAAGACGCTCAACAGCCTTAACCTCCGATGATATATGGA 114
QY 39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThraAspGlyThraSerThr 58
DB 115 AATGACCTTGAAGAGCTTCAAGGTAAAGAAAGAACTTATCA-----GAAACAAGTAT 168
QY 59 ValPheLysAspSerValValL1eGlnAenValProLysThrGlyLysThrGlnSerThr 78
DB 169 ACTGTGAAGCAATGTGTATCTCTTTCGAGGAAAGATTCAGAGCTTAAGAAA--- 225
QY 79 SerCysPheLysAsnAspAlaL1eAlaGlyAenLeuAenPheLeuGlyLysGlyPheSer 98
DB 226 AGTTGTTTC-----TCAGCTAGTAATTAACCTTACCTCTCTAGAAACGGTATACT 276
QY 99 PheThrPheSerAenL1eAspAlaThrThraLysSerGlyAlaL1eGlySerGlnAla 118
DB 277 CTTCCTTGAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 336
QY 119 AlaAenLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
DB 337 CAGAGAAAACCTTAGGATCTCAGATTTTCTTATTTTCAATGCTTATTTGCTTCA 396
QY 139 SerThrValThraGlyLysGlyAlaL1eAenValLysGlyAsnLeuSerLeuLeuAap 158
DB 397 GGC-----ACAACTGTTACGAGCTATACAGATTAAGGCAACAACCTTTAAAGAT 450
QY 159 AenAspLysValLeuL1eGlnAenPheSerThrThraAspGlyLysGlyAlaL1eAenCys 178
DB 451 AACTGATGCTTGTCTTCATTAATAAAGCTTCAACAGCAAGAGGTGGGCTATTCAGTGT 510
QY 179 AlaGlySer-----LeuLysL1eAlaAenLysSerLeuSerPheL1eGly 194

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Db      511 AAAGAGACAGTGAAGCTGAATTAATAATAGAAATAATCAAGAACTGTTTTCAGAA 570
Oy      195 AenSerSerThrArgGlyValIleHisThrIleValSerLeuThrSerSerGly 214
Db      571 AACTCTCTCACTTCAAAAGCGGGACCTTTATAGCTGATTAACATCAACATGTCACAGT 630
Oy      215 GlyIuThrLeuPheGlnGlyValSerThrAlaProThrAlaAlaGly---LysGlyValAla 233
Db      631 GGGCTACATATTATTCTAACAACCTGTATCCAAAGGTTATCCCTTAAGGCGAGACT 690
Oy      234 IleAlaIleAlaSer---SerGlyThrLeuSerIleSerGlyAspSerGlyAspIleIle 252
Db      691 ATTGACATTAAGATTCAAGTGTGAATGTAGCTTACCGCTGATCTGGAGATTATCC 750
Oy      253 PheGlnGlyAsn-----ThrIleGlyAlaThrGlyThrValSerHisSerAla 268
Db      751 TTCATGGGAACCAATCATCAAACTAGTGTGAGAGTTCTTACGTAAACAGAAATTC 810
Oy      269 IleAspLeuGlyThrSerAlaValIleThrAlaLeuAlaAlaGlnGlyHisThrIle 288
Db      811 ATAGATCTCGGACAC---GGGAAATTTCAAAGCTACGCTTAAAGACGCTTCGAGATT 867
Oy      289 TyrPheTyrAspProIleThrValIleThrGlySerThrSerValAlaAspAlaLeuAsnIle 308
Db      868 TTCCTCTATGACCCCTATTACTGGGGAGAGATCT-----GATGAATCAAAACAT 915
Oy      309 AsnSerProAspThrGlyAspAsnIleGlyIuThrGlyThrIleValPheSerGlyIu 328
Db      916 AATTAATAAAGAAACCTGTGAT-----TATACAGAAAGATGCTTCTTCAGGTAA 966
Oy      329 LysLeuThrGluAlaGluAlaValAspGlyIuValAsnArgThrSerLeuLeuGlnAsn 348
Db      967 AATATTATCCGATGAAGAAAGAAAGACAGAGCGAAACCTAGCTTCACTTCAACCAACC 1026
Oy      349 ValAlaIleValSerGlyThrValIleLeuGlyValAspValValLeuSerAlaAsnGly 368
Db      1027 ATCATTATATGACGAGATCTCTTCTACTTAAAGATGTGTATCTGTAACCGCAAAACA 1086
Oy      369 PheSerGlnAspAlaAsnSerLeuIleMetAspLeuGlyThrSerLeu----- 385
Db      1087 GTAAAGCGAAGAGCGGATCTACCGTGTCAATGATCTAAGGACCAATTCACAGCGCT 1146
Oy      386 ValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSerLeuArg 405
Db      1147 TCTTCAGGTGAGAAACATCAACCTTACTATATGATTTAAATTAATGCGCTCGTTGGGG 1206
Oy      406 AsnGly-----LysLeuIleValSerAlaAlaThrAlaGlnLysAspIleArg 422
Db      1207 GGGGGGGGGGTACTCTCTGCTAACTCCGCAACAAATACAGCAAGTCAAGCTATACT 1266
Oy      423 IleAspArgProValValLeuAlaIleSerAspGlyIuSerPheTyrGlnAsnGlyPheLeu 442
Db      1267 ATTAAC---GCTGTAACTAGTCAATGCTGATGTGCAATGCTTAAGAAATCTTAATCTT 1323
Oy      443 AsnGluAspHisLeuSerTyrAspGlyIleLeuGluLeuAspAlaGlyLysAspIleValIle 462
Db      1324 GCTACGTAAACCTTTCACAGCATATGATGATCACTAAGCTAAGCTAAGTCAACAG 1383
Oy      463 SerAlaAspSerArgSerIleAspAlaValGlnSerProTyrGlyTyrGlnGlyLysTyr 482
Db      1384 CCTACAGATTAATCTAACAATATATGCTCTCTACTACTACATTAAGGTTACCAAGAAATGG 1443
Oy      483 ThrIleAsnTyrSerThrAsp-----AspIleValIleThrValSerThrAlaLysGln 500
Db      1444 ACAGTAACCTTGGACACGAAACAGCTACAAACCAACCAACCTTAAGTGGAAACAACT 1503
Oy      501 SerPheAsnProThrAlaGluGlnGluAlaProLeuValProAsnLeuLeuTyrPheSer 520
Db      1504 GGCTACTCCCTTAACCAAGAGTCAAGAGACCTTTATAGTCCGAATATCTTTGGGGTCA 1563
Oy      521 PheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGlyAlaProTyr 540

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Db      1564 TTCCTGACCTCAGAGCTATACAAACTTAATGATATTAAGCTCAATGGCGTCACTAC 1623
Oy      541 GluIuAspPheThrPValAlaGlyIleSerAsnValLeuHisArgSerGlyArgIuAsn 560
Db      1624 CATAGAGTTTGGGATATCCGCTGACATCTTCTTACCAAAAGTGGCTGATACT 1683
Oy      561 GlnArgIuPheArgHisValSerGlyValAlaValAlaGlyAlaSerThrArgMetPro 580
Db      1684 AACCGCAAGTCCGTCACAAATAGCGCGGATACGCTTAAAGCGCTACGCAAAACCTCT 1743
Oy      581 GlyIuAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspIleAspTyrPhe 600
Db      1744 TCTGATATATTTCACTGCGCTTCTGCGCACTCTTGGAAAGACAAAGACTATTTA 1803
Oy      601 MetAsnThrAsnPheAlaValThrTyrAlaGlySerLeuArgLeuGlnHisAspAlaSer 620
Db      1804 GTTCGAAACCAACCGCAACATTTACGAGGTTCTCTATTTATCAGAT--ATCTCC 1860
Oy      621 LeuTyrSerValValSerIleLeuLeuGlyGluGlyLeuArgGluIleLeuLeuPro 640
Db      1861 TATTGAGC-----GCTTGGCAAGAACTCTCAACAAAC 1893
Oy      641 TyrValSerIuThrLeuProCysSerPheTyrGlyIuLeuSerTyrGlyHisThrAsp 660
Db      1894 ACTATCGGTGAGAGCTCCGTTAGTCTTAACGCAAGTTATGTCATGCTTCA 1953
Oy      661 HisArgMetLysThrGlu-----SerLeuProProProProThrLeuSerThr 677
Db      1954 AACGACATGAACCAACATGACACATTAACGCTCTCTGTAACCAATGACGAA 2013
Oy      678 AspHisThrSerTyrGlyIuTyrValIleAlaGlyIuLeuGlyThrArgValAlaVal 697
Db      2014 ATCAAGGGATGTTGGGATACGATGTTTGGAGTTCGAGCTGAGTGCACATGCTCATC 2073
Oy      698 GluAsnThrSerGlyArgGlyPhePheGlnGluIuTyrThrProPheValIleGlnAla 717
Db      2074 CAACAGAAATTTCTCTC--CTATTGATATGATACACCTTCTCGAACTTCACTT 2130
Oy      718 ValTyrAlaArgGlnAspSerPheValIleLeuGlyAla---IleSerArgAspPheSer 736
Db      2131 GTGCATACGACCAAGATGACTTTAAGAAACATATGCGATCAGGAAATACTTGGAA 2190
Oy      737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleLysLeuGluIuLysArgPheAla 756
Db      2191 AGCAGCAATCTCAACCACTTCTCTGCTATGCGATCAAGTTGAG--AGATTGGCT 2247
Oy      757 GluGln-----TyrTyrHisValAlaAlaMetTyrSerProAspValCysArgSer 773
Db      2248 AACCAAGATACAGCTTCTTATCATGTCACTGCTCTTAATCTCTGATATGTAAGAGT 2307
Oy      774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer-----TyrLysThrLys 791
Db      2308 AACCTGACTGATCTACTCTCTGTAGTAAGCCCCCACTGCTGCTGGTAAAGAA 2367
Oy      792 GlySerAsnLeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGly 811
Db      2368 GCCAACAACCTTGGCGAAGCGCTTATGCTAACAACAGAAACTTCTTTAAGT 2427
Oy      812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyrArgIuLysSerArgSerTyr 831
Db      2428 CACAACAATAGAAATCTTACAGCACTGCGTTTCCAGCTCAAGGGGATCTTCAAGAACTAT 2487
Oy      832 AsnValAspAlaGlySerLysIleLysPhe 841
Db      2488 AACTGATCTCGGATCGAAGATCCAGTTC 2517

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RESULT 5

US-10-023-437-22

; Sequence 22, Application US/10023437

; Publication No. US20020183272A1

; GENERAL INFORMATION:

; APPLICANT: JOHNSTON, STEPHEN A.

; APPLICANT: STEMBER-HALE, KATHERINE

APPLICANT: SYKES, KATHRYN F.
 APPLICANT: KALTENBOECK, BERNHARD
 TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING NUCLEIC ACID
 TITLE OF INVENTION: AND/OR POLYPEPTIDE SEQUENCES OF CHLAMYDIA
 FILE REFERENCE: UTSD:736US
 CURRENT APPLICATION NUMBER: US/10/023,437
 CURRENT FILING DATE: 2001-12-17
 PRIOR APPLICATION NUMBER: 60/225, 839
 PRIOR FILING DATE: 2000-12-15
 NUMBER OF SEQ ID NOS: 69
 SOFTWARE: PatentIn Ver. 2.1
 SEQ ID NO 22
 LENGTH: 2520
 TYPE: DNA
 ORGANISM: Chlamydia petfecti
 US-10-023-437-22

Alignment Scores:
 Pred. No.: 3,15e-143 Length: 2520
 Score: 1497.00 Matches: 357
 Percent Similarity: 56.21% Conservative: 132
 Best Local Similarity: 41.03% Mismatches: 321
 Query Match: 34,854 Indels: 60
 DB: 14 Gaps: 25

US-09-830-446-27 (1-841) x US-10-023-437-22 (1-2520)

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QY      1 MetLysIleProLeuArgHleuLeuIleSerLeuValProThrIleuSerMetSerAen 20
DB      1 ATGAAACATCGAGTCTAGCTGTTCTTAATATCC-----TCGAGCTTATTTGGCTCGAAT 54
QY      21 LeuLeuGlyAlaAlaThrThrgluGlu-----LeuSerAlaSerAenSerPheAsgly 38
DB      55 TCTTTAGAGTTCGCTAACGACGCTCAACGCTTAACCTCCCTCCATACCTATATGGA 114
QY      39 ThrThrSerThrThrSerPheSerSerLyThrSerSerAlaThrAaspGlyThraeny 58
DB      115 AATGTGACCTCGAGGAGTTCACGATTAAGAAAGAACTTCATCA-----GGAACACGATAT 168
QY      59 ValPheLyAaspSerValIalleGluAenValProLyThrGlyIuhThrgInSerThr 78
DB      169 ACTGTGAAAGGCAATGTGTATCTCTTTCGAGGAAAGATTCAAGCTTAAGAA---- 225
QY      79 SerCyPheLyAaspAlaAlaIleAglYaspLeuAenPheLeuGlyGlyGlyPheSer 98
DB      226 AGTGTGTTCT-----TCAGCTACTGATTAACCTTAACCTTCTTACGAAACGGGTACT 276
QY      99 PheThrPheSerAenIleAaspAlaThrThraIaSerGlyAlaAlaIleGlySerGluAla 118
DB      277 CTTTGCTTGATTAATTAATACTACTACAGCTAGTAACCCGAGCATTAATGTTCAAGGT 336
QY      119 AlaAenLyThrValThriLeuSerGlyPheSerAlaLeuSerPheLeuLySerProAla 138
DB      337 CAAGGAAACCTTAGCAGATCTCAGAGATTTCTTAATTTTCATGTCCTAATGTTCTTCCA 396
QY      139 SerThrValThraAenGlyLeuGlyAlaIleAenValIleGlyAenLeuSerLeuAenP 158
DB      397 GGC-----ACACTGATCTGTCTTCAATAAAACGTCTCAACGAGAAAGTGGGCTATCCAGT 450
QY      159 AenAaspLyValLeuIleGlnAenAenPheSerThrGlyAaspGlyGlyAlaIleAenCy 178
DB      451 AACTGATGCTGTCTTCAATAAAACGTCTCAACGAGAAAGTGGGCTATCCAGT 510
QY      179 AlaGlySer-----LeuLyGlyIleAlaAenAenLySerLeuSerPheIleGly 194
DB      511 AAAGGAGGAGTGTCTGAATTAATAAATAAATAATCAGATCTGCTTTCTCAGAA 570
QY      195 AenSerSerThrArgGlyGlyAlaIleIleThrLyAenLeuThriLeuSerSerGly 214
DB      571 AACTCTTCACTCAAAAGCGGGCTATTTATGCTGATTAACCTCAACCATGCTCAAGT 630
QY      215 GlyGluThrLeuPheGlnGlyAenThrAlaProThrAlaIleGly---LyGlyGlyAla 233
  
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DB      631 GGGCTACATTAATTTCTTAACAACCTGTATCCAAAGGTTCAATCCCTTAAGCGGAGCT 690
QY      234 IleAlaIleAasp---SerGlyThriLeuSerIleSerGlyAaspSerGlyAaspIleIle 252
DB      691 ATTAGCATTAAGATTTCAAGTGTGATGTATGATCTTAACCCGCTGATTCGAGATATTTACC 750
QY      253 PheGlyLyAen-----ThrIleGlyAlaThrglyThraIaSerIleSerAla 268
DB      751 TTCGATGGGAACAAATCATCAAAACCTAGTGTGGAAGTTCAAGTATCAAGAAATTC 810
QY      269 IleAepLeuGlyThraSerAlaLyIleThraIaLeuAlaGlnGlyIleThriIle 288
DB      811 ATAGATCTCGGACA---GGAAATTTCAAAAGCTTACGCTTAAGACCGCTTCGGAAAT 867
QY      289 TyrPheTyraPProIleThraValThrglySerThrSerValAlaAaspAlaLeuAenIle 308
DB      868 TTCCTCTATGACCTTAATTAATCGGGGAGGATCT-----GATTAACCTTAACATT 915
QY      309 AenSerProAepThrGlyAaspAenLyGlyTyThrGlyThriLeuValPheSerGlyGlu 328
DB      916 AATTAAGAAAGAAACGTTGAT-----TATACGAGAAAGATGCTCTTCAGGTGA 966
QY      329 LybLeuThrgluAlaGluAlaLyAaspGlyLybAenAsgThriSerLybLeuGlnAen 348
DB      967 AATTAATCCGATGAAGAAAGAAACGAGCGGAAACCTAGCTTCTTCAACCAACCC 1026
QY      349 ValAlaPheLyAenGlyThraValIalleuLyGlyAaspValIleuSerAlaAenGly 368
DB      1027 ATCACTATTAACGACGAGATCTTGTACTTAAGATGTGTATCTGTAAACCCGAAAAA 1086
QY      369 PheSerGlnAaspAlaAenSerLybLeuIleMetAepLeuGlyThriSerLeu----- 385
DB      1087 GTAAGCGAGGAAGCGGAGATCTACCGTTGATGATGATGATGATGATGATGATGATGAT 1146
QY      386 ValAlaAenThrgluSerIleGluLeuThraAenGlyIleAenIleAaspSerLeuAsg 405
DB      1147 TCTTCAAGTGAAGAAACCATCACTTAATCTAGATTAATTAACATCCCTCGTTGGGG 1206
QY      406 AenGly-----LybLyIleLybLeuSerAlaAlaThraIleGlnLybAaspIleAsg 422
DB      1207 GGGGGGGGGGTAACCTCTCTCTTAACCTCGCAACAATACGAAAGTAACCTTAACCT 1266
QY      423 IleAaspArgProValIleAenAlaIleSerAepGlySerPheTyrcGlnAenGlyPheLeu 442
DB      1267 ATTAAC---GCTGTCAATCTACTGATGCTGATGCGAATGCTTATGAAGATCTTATCTT 1323
QY      443 AenGluAepHleSerTyraPglyIleLeuGluLeuAaspAlaGlyLybAaspIleValIle 462
DB      1324 GCTAGCTTAACCTTTCACAGCAATAGAGCTCACTTAACGCTAGTACAGTCAACAG 1383
QY      463 SerAlaAaspSerArgSerIleAaspAlaValAenSerProTyrcGlnGlyIleYstrP 482
DB      1384 CCTACAGATTAATCAACAATTAATGTCTCTACTCACTTAAGGTATACGAAAGAAATG 1443
QY      483 ThrIleAenTrpSerThraP-----AepLybLybAlaThraValSerTrpAlaYsgIn 500
DB      1444 ACGATTACTTGGGACACCGAAACAGCTACAAABAACGACCTTAACCTTGGGAAACAACT 1503
QY      501 SerPheAenProThraIleGlnGluAlaProLeuValProAenLeuThriGlySer 520
DB      1504 GGCTACTCCCTTAACCCAGAAAGCTCAAGGACCTTAATGTCGAAATATCTTTGGGGTGA 1563
QY      521 PheIleAepValArgSerPheGlnAenPheIleGluLeuGlyThrgluGlyAlaProTy 540
DB      1564 TTCTGTACCTCAGAGCTTAACAAACTTAAGATATTAAGGCTCAATGCGCTGACATAC 1623
QY      541 GlybAsgPheThraValAlaGlyIleSerAenValIleuHleAsgSerGlyArgGluAen 560
DB      1624 CATTAAGGTTTGGGTATCCGCTAGCTAATCTTACCAAAAGTGGCTGTATCTACT 1683
QY      561 GlnArgLybPheAsgHleAenSerGlyGlyAlaValAlaGlyAlaSerThraArgMetPro 580
DB      1684 AAACCAAGTTCGTCACAAATAGCGCCGATACGCTTATGAGCGGTCAACAAAACTCCT 1743
  
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Qy 581 GlyIysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAspTyrPhe 600
Db 1744 TGTATGATATTTTCAAGTGGGCTTTCGCCAACTCTTCGAAAGACAAAGACTATTTA 1803
Qy 601 MetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuAspGlnHisAspLysSer 620
Db 1804 GTGTGAAAAACCAAGCCCAACATTTACGAGGTTCTCTATATATACAGAT---ATCTCC 1860
Qy 621 LeuTyrSerValIleSerIleLeuLeuGlyGlyGlyLeuAspGlnIleLeuLeuPro 640
Db 1861 TATTGAGC-----GCTTGGCAAAATCTGCTACAAAC 1893
Qy 641 TyrValSerIleThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGlyHisThrAsp 660
Db 1894 ACTATCGGAGCAAGAGCTCCGTTAGCTCTTAAGCAAGTTAACTTATGTCATGCTTCA 1953
Qy 661 HisArgMetIleThrGln-----SerLeuProProProProProThrLeuSerThr 677
Db 1954 AACGACATGAAAAACCAACATGACGACTACTACGCTCCCTGTAACCAACATGATGACGA 2013
Qy 678 AspHisThrSerThrGlyGlyTyrValTyrAlaGlyGlyLeuGlyThrArgValAlaVal 697
Db 2014 ATCAAGGCTGATGAGGTAACCATGTTTCGAGATCGAGCTTGCGCACTGTGCTCTATC 2073
Qy 698 GlnAsnThrSerGlyArgGlyPhePheGlnGlyTyrThrProPheValIleValAla 717
Db 2074 CAACAGATCTTCTCTC---CTATTGATATGATCTACCTTCTGTAAGTTTCACTT 2130
Qy 718 ValTyrAlaArgGlnAspSerPheValGlyLeuGlyAla---IleSerArgAspPheSer 736
Db 2131 GTCGATACGCAACCAAGATGACTTAAAGAAACAAATAGCATCAGGAAAGATATCTCGAA 2190
Qy 737 AspSerHisLeuTyrAsnLeuAlaIleProLeuGlyIleValLeuGlnIleValArgPheAla 756
Db 2191 AGCAGAAATCTACCAACTTCTCTGCTATCGGATCGGATCAAGTTTGA---AGATTGCT 2247
Qy 757 GlnGln-----TyrTyrHisValAlaIleMetTyrSerProAspValCysArgSer 773
Db 2248 AACACGATACAGCTTCTTATCATGCTACGCTGCTTATCTCTGATATGCTGAAGAGT 2307
Qy 774 AsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySer-----TyrLysThrLys 791
Db 2308 AACCTGACTGACTACTCTCTCTGTAGTACGCCGACCTGCTGTGCGGTAAACGAA 2367
Qy 792 GlySerAsnLeuAlaArgGlnAlaGlyIleValAlaSerGlyPheArgSerLeuGly 811
Db 2368 GCCAACACCTTCGCGAGCGCTTCATGCTACAGCAAGAACTACTTCTTTAAGT 2427
Qy 812 AlaAlaAlaGlyLeuPheGlyAsnPheGlyPheGlyTyrPyrGlySerSerArgSerTyr 831
Db 2428 CACAACATAGAAATCTTCAGCGCATTCGCTTCGAGCTCAGGGGATCTTCAAGAACTAT 2487
Qy 832 AsnValAspAlaGlySerIleIleLysPhe 841
Db 2488 AACGTAGATCTCGATCGAAGATCCAGTTC 2517

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RESULT 6
US-10-312-273-116

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/ Sequence 116, Application US/10312273
/ Publication No. US20040005667A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
/ FILE REFERENCE: P025035WO
/ CURRENT APPLICATION NUMBER: US/10/312,273
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 0016363.4
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 0017047.2
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 0017983.8
/ PRIOR FILING DATE: 2000-07-21

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/ PRIOR APPLICATION NUMBER: 0019368.0
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: 0020440.4
/ PRIOR FILING DATE: 2000-08-18
/ PRIOR APPLICATION NUMBER: 0022583.9
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 0027549.5
/ PRIOR FILING DATE: 2000-11-10
/ PRIOR APPLICATION NUMBER: 0031706.5
/ PRIOR FILING DATE: 2000-12-22
/ NUMBER OF SEQ ID NOS: 664
/ SOFTWARE: SeqWin99, version 1.02
/ SEQ ID NO 116
/ LENGTH: 2787
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ US-10-312-273-116

Alignment Scores:
Pred. No.: 7,71e-137 Length: 2787
Score: 1435.50 Matches: 340
Percent Similarity: 51.43% Conservative: 147
Best Local Similarity: 35.90% Mismatches: 335
Query Match: 33.42% Indels: 125
DB: 12 Gaps: 15

US-09-830-446-27 (1-841) x US-10-312-273-116 (1-2787)
Qy 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db 1 ATGAAGACTTCGATTCCTTGAGTTTACTTCTCCGTTAGCTTCTCA---TGTCAC 57
Qy 21 LeuLeuGlyAlaAlaThrThrGlyGlyLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db 58 CTACAGTACAGTACAGTACAGAGAACTTTATCACTGATATGATGTTTAATGAAGAAATATC 117
Qy 41 SerThrThrSerPheSerSerLysThrThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60
Db 118 GATTCAGGAGAGCTTATCCAAAACCTTCAGCC-----ACAAATATATCTCTTA 165
Qy 61 LysAspSerValIleGlnAsnValProLysThrGlyGlnThrGlnSerThrSerCys 80
Db 166 ACGAGAGATGCTCTTCTTTTACAG---CTGGAAAGCACTCCTTATGACAGTTGT 222
Qy 81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPheSerPheThr 100
Db 223 TTTAAGCAA-----ACCAAGCAATCTTACCTTCTGGGAAAGGTCATAGCTTAAG 276
Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlnAlaAsn 120
Db 277 TTTGGCTTTATATGATGCTGCGACATCATCAGGTGCTGCT---GCATCTTAACAAGCAAT 333
Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
Db 334 AAGAACTTACCTTCTCGAGGTTTCTTACTGAGTTTGAATTCCTCTTCGACCAACG 393
Qy 141 ValThrAsnGlyLeuGlyAlaIleAsnValIleGlyAsnLeuSerLeuLeuAspAsnAsp 160
Db 394 GTTACTACAGGTCAAGGAAAGCGTTTCTCAGCAGAGAGCGTAAATTTGAAATATTTGT 453
Qy 161 LysValLeuIleGlnAspAsnPheSerThrGlyAspGlyGlyAlaIleAsnCysAlaGly 180
Db 454 AAACCTGTAGTTGCTGGAAATTTTCTACTGACAGATGCTGAGGCTATCAAGAACGCTCT 513
Qy 180 ----- 180
Db 514 TTCCTTTAAGTGGACTTTCGAGATGCTCTTTTATGTAACAACCTTCAACAAG 573
Qy 180 ----- 180
Db 574 GAGAGCAATTTGCTACTACAGCAGCGCTGCAATAGCAATTAACAAGTTATGTAGA 633
Qy 180 ----- 180

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Db 634 TTCCTATCTAACTACGCTCTACGAGAGCGCTATGATGATGAGGACGCTGATA 693
 QY 180 ----- 180
 Db 694 CTATGGAACAAATTTCTATATTTTGAAGGAGATGACGGAATACTAGCGGTGG 753
 QY 181 -----SerLeuLysIleAlaAsnLysSerLeu 190
 Db 754 ATCTGCACACCAAGCGAGTGATCTCTGAACTGATATCTCTAACTAATAGACTCTG 813
 QY 191 SerPheIleGlyAsnSerSerThrArgGlyValIleHisThrLysAsnLeuThr 210
 Db 814 ATCTTGCTTCAACCTAGCAAGAAACAGCGGTGGCCATCCATCTTAAAGCTAGCC 873
 QY 211 LeuSerSerGlyGlyLeuThrLeuPheGlnGlyAsnThrAlaProThrAlaIleGlyLys 230
 Db 874 CTTTCTCTGAGGCTTTACAGAGTTTCAAGAAATATGTCATCAGCACTCTTAAG 933
 QY 231 GlyGlyValIleAlaIleAlaAspSerGlyThrLeuSerIleSerGlyAspSerGlyAsp 250
 Db 934 GGGGGGTCTATGACATCGATCGCTCAGAGAGCTCAGTCTTCTGACAGACAGAAAC 993
 QY 251 IleIlePheGlnGlyAsnThrIle-----GlyAlaThrGlyThrValSerHisSer 267
 Db 994 ATTACCTTGTAAGAAATACCTTACACAAACCGGAAGTACGATCTCTTAAACGTAT 1053
 QY 268 AlaIleAspLeuGlyThrSerAlaLysIleThrAlaLeuArgAlaIleGlnGlyHisThr 287
 Db 1054 GCGATCAACATGAGAGTAAACCGGAAATTCACCGAATTACGGCTCTTAAATCTTACA 1113
 QY 288 IleThrPheThrAspProIleThrValThrGlySerThrSerValAlaAspAlaLeuAsn 307
 Db 1114 ATTTCTCTCATGATCCCATCTCTCAGAAAGAACTCATCA-----GACGATATGAG 1167
 QY 308 IleAsnSerProAspThrGlyAspAsnLysGlyThrGlyThrIleValPheSerGly 327
 Db 1168 ATTAATAACGGCTCTGCGGAGCTCTCAATCCATATCAAGAAACGATTTCTATTTCTGA 1227
 QY 328 GlyLysLeuThrGlyLysIleGlnAlaLysAspGlyLysAsnArgThrSerLysLeuLeuGln 347
 Db 1228 GAACCTTAACAGCATGATTAATAGTTGCTGACAAATTTAAATCTTCAATTCACGAG 1287
 QY 348 AsnValAlaPheLysAsnGlyThrValIleLeuLysGlyAspValIleLeuSerAlaAsn 367
 Db 1288 CCAAGTCTCCCTAACCGAAGAAAGTATGCTTACAAAGGAGCTCACTTAAAGACAG 1347
 QY 368 GlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeuValAla 387
 Db 1348 AGCTTCTTCAAGAGCGCGGTCTCTCTCGCATGATTCAGAAACGACATTATCACT 1407
 QY 388 AsnThrGlnSerIleGlyLeuThrAsnLeuGlnIleAsnIleAspSerLeuArgAsnGly 407
 Db 1408 ACAAGCTGGAGATTTCAATCAAGAACTTAGAAATCAATGATGACTCTTAAGCTTAAAG 1467
 QY 408 LysLysIleLysLeuSerAlaAlaThrAlaGlnLysAspIleArgIleAspArgProVal 427
 Db 1468 CAGCCCTCAGCTTAACAGAAAGGCTTCAAAATAAGTATGCTAATCTGGAGAGCTC 1527
 QY 428 ValLeuAlaIleSerAspGlySerPheTyrgLysAsnGlyPheLeuAsnGlyLysAspHisSer 447
 Db 1528 AACCTATGATATTAAGGAAACATTTATGAAAGTCATATGTTCCAGCATGACGAGCTC 1587
 QY 448 TyrAspGlyIleLeuGlyLeuAspAlaGlyLysAspIleValIleSerAlaAspSerArg 467
 Db 1588 TTC---TCTCTATTAATAATCACGCTTGATGCTGAGTATCTAAGCTGATCAGC 1644
 QY 468 SerIleAspAlaVal-----GlnSerProGlyTyrgLysGlyLysLeu 482
 Db 1645 AGCTTATCCCTGTTCTGCTGAGATCTTAATTCAGAAATAGAGATTCAGAGCAATG 1704
 QY 483 ThrIleAsnThrSerThrAsp-----AspLysLysAlaThrValSerThrAla 498

Db 1705 AATGTTAATGGACTACGATACAGCTACAAATACAAAAGAGCCAGCGCACTTGAGACC 1764
 QY 499 LysGlnSerPheAsnProThrAlaGlnGlnGlyAlaProLeuValProAsnLeuLeuTyr 518
 Db 1765 AAAACAGATTTGTTCCAGCCCCGAAAGAAATCTGCGTTATGATGCAATACCTATGG 1824
 QY 519 GlySerPheIleAspValArgSerPheGlnAsnPheIleGlnLeuGlyThrGlnGlyAla 538
 Db 1825 GGAAGCTTACTGACATTCGCTCTGCAACAGCTTGATGAGATCGGCCCACTGGTATG 1884
 QY 539 ProTyrgLysArgPheThrValAlaGlyIleSerAsnValLeuHisArgSerGlyArg 558
 Db 1885 GAACAAACAAAGGTTCTGGGTTTCTCCATGACGAACCTTCTGCTAAGACTGAGAT 1944
 QY 559 GlnAsnGlnArgLysPheArgHisValSerGlyGlyAlaValAlaGlyLysSerThrArg 578
 Db 1945 GAAATTCGAAAGGCTTCGCTCATACCTGAGAGCTACGATCATCGGTGAGATGCTCAC 2004
 QY 579 MetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLysAsp 598
 Db 2005 ACTCTTAAAGACGACTATTTACCTTGGCTTCCCATCTCTTGTGAGACAAAGAT 2064
 QY 599 TyrPheMetAsnThrAsnPheAlaLysThrTyrgLysSerLeuArgLeuGlnHisAsp 618
 Db 2065 TGTTTATGCTCACAACTCTGAACTTACGCTGAGAACTTATCTTCAAGCACTCT 2124
 QY 619 AlaSerLeuTyrgSerValSerIleLeuLeuGlnGlyGlyLysArgGlyLeuLeu 638
 Db 2125 CATACCTTAACAAACCCAAACATTTAGATTAGGAAGACAAAGTTTCTGAATCAGCT 2184
 QY 639 LeuProTyrgValSerLysThrLeuProCysSerPheTyrgLysGlnLeuSerTyrgLys 658
 Db 2185 ATAGAAATAATCCCAAGGAAATTCCTTGAAGTCCCTGATGATCCAAAGTTTCTGACGCCAT 2244
 QY 659 ThrAspHisArgMetLysThrGln-----SerLeuProProProProThrLeuSer 676
 Db 2245 TCAGACAAACGATGAGAAACGCACTATACCTCATTTGCCA----- 2283
 QY 677 ThrAspHisArgSerTyrgLysTyrgValAlaThrAlaGlyLysLeuGlyThrArgValAla 696
 Db 2284 GAATCGGAAGCTCTTGGAGCAACAGATGATAGCTGGTGGATGAGCGCTTACCTCT 2343
 QY 697 ValGlnAsnThrSerGlyArgGlyPhePheGlnGlyTyrgThrProPheValLysValGln 716
 Db 2344 TTGTGCTTCCCAACCCACATCTCTTCAAGACCTTCAATTCACAGATGAAGCGAA 2403
 QY 717 AlaValTyrgAlaArgGlnAspSerPheValGlnLeuGlyAlaIleSerArgAspPheSer 736
 Db 2404 ATGGTTATGATCACAAAATAGCTTCTTGAAGCTTAGATGAGCCGCTGGTTTACT 2463
 QY 737 AspSerHisLeuTyrgAsnLeuAlaIleProLeuGlyLysLeu---LeuGlnLysArgPhe 755
 Db 2464 ATTGGAAGCTCTTAACCTTCGATTCCTGCTGGGTGCAAAATTCGTGAGGGGAGATTC 2523
 QY 756 AlaGlnGlnTyr---TyrgHisValAlaMetTyrgSerProAspValCysArgSerAsn 774
 Db 2524 GGAAGATCTCAACCTATGATCTCTCAGGATCTTGTGTTCCGAGTGTATGTAACAT 2583
 QY 775 ProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTyrgLysThrLysGlySerAsn 794
 Db 2584 CCCCAATCTACAGCACTCTTGATGAGCCCAAGCTCTTGAATAATTCGCGGTGGCAAT 2643
 QY 795 LeuAlaArgGlnAlaGlyIleValGlnAlaSerGlyPheArgSerLeuGlyAlaAlaAla 814
 Db 2644 CTTTCAAGACAGCACTTTTACTGAGGGGTACCAACAATAGCTACAACTCCAACTTGT 2703
 QY 815 GlnLeuPheGlyAsnPheGlyPheGlnTyrgArgGlySerSerArgSerTyrgAsnValAsp 834
 Db 2704 GAGCTTCTGCAATTAACCTATGAAACCTGTGATCTTCAAGAACTACATGATGAT 2763
 QY 835 AlaGlySerLysIleLysPhe 841
 Db 2764 GTTGTACCAACCTCGATTC 2784

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RESULT 7
US-10-312-273-46
; Sequence 46, Application US/10312273
; Publication No. US200400567A1
; GENERAL INFORMATION:
; APPLICANT: CHIRON SPA
; TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
; FILE REFERENCE: P025035W0
; CURRENT APPLICATION NUMBER: US/10/312.273
; CURRENT FILING DATE: 2002-12-20
; PRIOR APPLICATION NUMBER: 0016363.4
; PRIOR FILING DATE: 2000-07-03
; PRIOR APPLICATION NUMBER: 0017047.2
; PRIOR FILING DATE: 2000-07-11
; PRIOR APPLICATION NUMBER: 0017983.8
; PRIOR FILING DATE: 2000-07-21
; PRIOR APPLICATION NUMBER: 0019368.0
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 0020440.4
; PRIOR FILING DATE: 2000-08-18
; PRIOR APPLICATION NUMBER: 0022583.9
; PRIOR FILING DATE: 2000-09-14
; PRIOR APPLICATION NUMBER: 0027549.5
; PRIOR FILING DATE: 2000-11-10
; PRIOR APPLICATION NUMBER: 0031706.5
; PRIOR FILING DATE: 2000-12-22
; NUMBER OF SEQ ID NOS: 664
; SOFTWARE: Seqwin99, version 1.02
; SEQ ID NO 46
; LENGTH: 2793
; TYPE: DNA
; ORGANISM: Chlamydia pneumoniae
US-10-312-273-46

Alignment Scores:
Pred. No.:      8,79e-135      Length:      2793
Score:          1415.50        Matches:      352
Percent Similarity: 50.53%      Conservative: 129
Best Local Similarity: 36.97%    Mismatches:   338
Query Match:    32.96%         Indels:       133
DB:             12             Gaps:         19
US-09-830-446-27 (1-841) x US-10-312-273-46 (1-2793)

Cy 1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20
Db 1 ATGAAATATACCTTGACAAACTCTGATCTCT-----TCGACTCTTGCACTCCCACT 54
Cy 21 LeuLeuGlyAlaIleThr-----ThrGluGluLeuSerAlaSerAsnSerPheAsp 37
Db 55 CTATTGACGATTGCACTTACGAGACAGATGCTTTATTCCTCCACGATAGCTTTAT 114
Cy 38 GlyThrThrSerThrThrSerPheSerSerlyThrThrSerSerAlaThrAspGlyThrAsn 57
Db 115 GGAGCGCGCGCTACCA---TTTACTCCAAATCTACAGCAGATGCCAATGCAAGCAAC 171
Cy 58 TyrValPheIleAspSerValIleIleGluLeuValProIleThrGlyIleThrGlnSer 77
Db 172 TATGCTTATACGAAATGCTATATTAACATGCTGGGAAA---GGCAGCATTAACA 228
Cy 78 ThrSerCysPheIleAsnAspAlaIleAlaIleAspLeuAsnPheLeuGlyGlyIlePhe 97
Db 229 GCGTCTCTCTTACGAA-----ACTACGGGTGATCTGACCTTTACGGAAGGAGATAC 282
Cy 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleIleGlySerGlu 117
Db 283 TCATTTCATTCACACACGATGATCGGGGTTCGAATGCAAGAGCTGCG---GCAAGCACA 339
Cy 118 AlaIleAsnIleThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuIleSerPro 137
Db 340 ACTGCTATTAAGACCTTAACATTCACAGGATTTTCAACCTTTCCTCATTCGACGCTCT 399

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Cy 138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIleAsnIleAsnLeuSerLeuLeu 157
Db 400 GGAACACTACAGTGTGCTTACGAGAAAAAGATACCTTAAAGTCTCAGAGAGGCTTAATCTTACC 459
Cy 158 AspAsnAspIleValIleIleGlnAspAsnPheSer----- 169
Db 460 GATAAATGAAAGCATTCCTTTAGCCAAACGCTCCAAATGAACTAAATCAATGCGCGA 519
Cy 169 ----- 169
Db 520 GCGATCACCAAAAACTCTTCTATTTCTGGGAATACCTCTTCTAATACCTTCACTAGT 579
Cy 169 ----- 169
Db 580 AATAGCGCAAAAAAATTAGGTGAGCGATCTATAGCTCTCGCGCTGCAAGTATTTACAGA 639
Cy 169 ----- 169
Db 640 AACACCGGCGCATGATCTTTATGATATTAAGAGAGAACTGGGGGTGGGGCTTGCGGC 699
Cy 169 ----- 169
Db 700 TTGAAAGCAGCTCTCGATTAATCAAAATAGCTCCCTTTTCTCTCGAAAAACATGCA 759
Cy 170 -----ThrGlyAspGlyGlyAlaIleAsnCys-----AlaGlySer 181
Db 760 ACAGATGCTGACAGGCAAGCGCGGCGCATTTATGTGAAAAACAGAGAGAGACTCTACT 819
Cy 182 LeuIleValIleAsnAsnIleValIleSerLeuSerPheIleGlyIleAsnSerSerThrArgGly 201
Db 820 CTTAATCTCTCTGAAATTAAGCTGACCTTCCGCGAGAACTCTTCAAGTAATCAAGGC 879
Cy 202 GlyValIleIleThrIleValIleAsnLeuThrLeuSerSerGlyGlyIleThrPheGlnGly 221
Db 880 GAGCAATCTGTGCGCCATGCTGATCTTTCGCTGCGCTGCGCCCTACCTATTTTCAAT 939
Cy 222 Asn---ThrAlaProThrAlaIleGlyIleValIleAlaIleAlaIleAspSerGly 240
Db 940 AATGATGCGCGGAACACAGCTGACGAGCAAGCGCGCTATTTGCAATTCGCGACTTGGA 999
Cy 241 ThrLeuSerIleSerGlyIleAspSerGlyIleIleIleGluGlyIleAsnThrIleGlyAla 260
Db 1000 TCTTAAGTCTCTCTGCAATCAAGAGACATCAAGTCTCTGCAACACTTCACTCA 1059
Cy 261 ThrGly-----ThrValSerIleSerAlaIleAspLeuGlyThrSerAlaIleIleThr 278
Db 1060 ACTTCCCGCGCCACATGACACGCAATGCTATCTACCTGGATGTCAGCAAAATTAACG 1119
Cy 279 AlaLeuArgAlaIleGlnGlyIleThrIleThrPheIleThrAspProIleThrValThrGly 298
Db 1120 AACTTAAGGAGCGCAAGGCGCAATCTATCTATTTCTATGATCCGATTT---GCATCTAAC 1176
Cy 299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnIleGlu 318
Db 1177 ACCACAGAGAGCTTCAAGCTTGTACCATCAACACCGGATACCACTGCGCTTTAGAT 1236
Cy 319 TyrThrGlyThrIleValIlePheSerGlyIleIleValIleThrGlyIleAlaIleAspGly 338
Db 1237 TATTCAGAACGATTTGATTTTCTGCGGAAAAGCTCTCTGACATGAGCAAGGAGCTCT 1296
Cy 339 LysAsnArgThrSerIleValLeuGluIleAsnValAlaIlePheIleAsnGlyThrValIleLeu 358
Db 1297 GATTAATCTTACATATTAATTAAGCAACATGTGCTCTAGGCTCTGGAACCTTGACACT 1356
Cy 359 LysGlyAspValIleValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerIleLeuIle 378
Db 1357 AAAGAAATGTCGATGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1416
Cy 379 MetAspLeuGlyThrSerLeuValAlaAsnThrGlyIleGlyIleThrAsnLeuGlu 398
Db 1417 ATGCAACCGAGAAACAAAGCTTAAGCAAGATCTAAGCTATCACTTACCAAACTTCTC 1476
Cy 399 IleAsnIleAspSerLeuArgAsnGlyIleValIleIleValIleSerAlaIleThrAlaGln 418

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QY 60 PheIysAspSerValIleGluAsnValProIysThrGlyIuThrGlnSerThrSer 79
 Db 175 CTGACAGGAGATATACCTGCGAAACCTT-----GGGATTCGGCAGCTTTAACG 225
 QY 80 -----CysPheIysAsnAspAlaIleAlaGlyAspLeuAsnPhelGlyIleGlyPhe 97
 Db 226 AAGGGTGTGTTTCTGACACTACGGAATCT-----TTAGCTTGGCGGTAAAGGGGTAC 279
 QY 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleGlySerGlu 117
 Db 280 TCATCTTCTTTTAAATATT-----AAGCTAGTCTGAAAGGCGCAGCACTT---TCGTGT 333
 QY 118 AlaIleAsnIysThrValThrIleuSerGlyPheSerAlaIleuSerPheIleuSerPro 137
 Db 334 ACAACTATTAATAATCTCTCCCTAACAGAAATTTTCAGACTTCTTCTTACCGGCCCA 393
 QY 138 AlaSerThrValIleu-----
 Db 394 TCATCGGTAAATCAACACCCCTCAGAAAGGTGCAATTAAATGAGGAGATCTTACA 453
 QY 143 -----AsnGlyLeu-----
 Db 454 TTTGATTAACAATGAACTATTATTATAACAAGATTACTGTGAGAAATGCGGAGCC 513
 QY 145 -----
 Db 514 ATTCTACCAAGAACTTTCTTTGAAAAACAGCAGGAGATGATTTCTTTGAAAGGAAT 573
 QY 145 -----
 Db 574 AAATCGACGCAACAGGAAAAAGTGGGCTATTGTGCTACTGTAAGTATGATATT 633
 QY 146 -----GlyAla 147
 Db 634 ACAAAATAATACGGCTCTACCTCTTCTGAACAATATTGCTGAAGCTGAGGTGAGCT 693
 QY 148 IleAsnValIysGlyAsnLeuSerLeuAsnAspIysValIleuIleGlnAspAsn 167
 Db 694 ATTAATACACAGGAACTGTACATTTACAGGAAATAGCTCTCTTGTATTTTTCGAAAT 753
 QY 168 PheSerThr-----GlyAspGlyGlyAlaIleAsnCysAlaGlySerLeuIysIle 184
 Db 754 AGTGTGACGCGACCGCAGGAAATGAGAGAGCTTTCTGAGAGATGCGAGTATACATA 813
 QY 185 AlaAsnAsnIysSerLeuSerPheIleGlyAsnSerSerThrArgIleGlyAlaIle 204
 Db 814 TCTGGAAATCAGAGGTAACTTTCTCAGGAAACCAAGCTGACTAATGCGGAGCCATT 873
 QY 205 HisThrIysAsnLeuThrIleuSerSerGlyGlyIuThrIleuPheGlnGlyAsnThrAla 224
 Db 874 TATGCTAAGAACTTACACTGCGCTTCCGGGGG-----GGGGGGGTATCT 918
 QY 225 Pro-----ThrAlaIleGlyIysGlyAlaIleAlaIle 236
 Db 919 CTTTCTTCAACATATATAGTCCAGAGTACCACTGCAAGGTAAATGAGGCCATTTCTATA 978
 QY 237 AlaAspSerGlyThrIleuSerIleSerGlyAspSerGlyAspIleIlePheGlnIuIysAsn 256
 Db 979 CTGGCAGCTGGAGAGTGTAGTCTTTCACAGAAAGGAGGACATTAACCTTCAATGGGAAT 1038
 QY 257 ThrIleGlyAlaThr-----GlyThrValSerHisSerAlaIleAspLeuIleThrSer 274
 Db 1039 GCCATTGTTGCACTACACCAACCAACTACAAAGAAATTCATTATGACATAGAGTACT 1098
 QY 275 AlaIysIleThrAlaIleuAlaIleGlnGlyIleThrIleIysPheIysAspProIle 294
 Db 1099 GCAAAAGATCACAATTTAGCTCAATATCTGGGCAATAGACTTTTCTTACCATCCGATT 1158
 QY 295 ThrValIuThrGlySerThrSerValIleAspAlaIleuAsnIleAsnSerProAspThrGly 314
 Db 1159 ACTGCTAATACGGCTGGGATTTCTACAGTACTTTAATCTCAATTAAGGCTATGCAAGT 1218

QY 315 AspAsnIysGlyIuThrIleValPheSerGlyIuIysLeuThrGluAlaGlu 334
 Db 1219 AATAGTACAGATATATAGTGGTGCATTTGTTTCTGTGAAAAAGCTCTCGAAGAGAA 1278
 QY 335 AlaIysAspGlyIysAsnAspThrSerIysLeuGlnAsnValAlaIlePheIysAsnGly 354
 Db 1279 GCAAAAGTTGCAACAACCTCACTTACCGTGAAGAGCGCTTACCTTACATGCGAGA 1338
 QY 355 ThrValIleuIysGlyAspValIleuSerAlaAsnGlyPheSerGlnAspAlaAsn 374
 Db 1339 AATTATGACTTAAACGTGGTGTACCTCGATACGAAAGCTTTACTACAGCCGGGCT 1398
 QY 375 SerIysLeuIleuIleAspLeuGlyThrSerLeuValAlaAsnThrGlnSerIleGluLeu 394
 Db 1399 TCTCTGTATTATGATGCGGGCACAAGTTAAAGCAAGTACAGAGAGTCACTTTA 1458
 QY 395 ThrAsnLeuGlnIleAsnIleAspSerLeuAsnGlyIysValIleIysLeuSerAla 414
 Db 1459 ACAGTCTTTCATTCCTGTAGACTTTTAGCGCAGAGGTAAAGAAAGTTGATATGCTGT 1518
 QY 415 AlaThrAlaGlnIysAspIleArgIleAspArgProValIleuAlaIleSerAspGlu 434
 Db 1519 TCTGACCAAGTAAATAATGTAGACCCCTAGTGTCCGATTTCTTTGATTAACCAAGG 1578
 QY 435 SerPheIysGlnAsnGlyPheLeuAsnGlnAspHisSerIysThrAspGlyIleuGlnLeu 454
 Db 1579 AATGCTTATGAATAATCAGACTTAGAATAAATCAAGACTT---TCATTTGTTCACCTC 1635
 QY 455 AspAlaGlyAspIleValIleSerAlaAspSerSerIleAspAlaValGlnSer 474
 Db 1636 TCTGCT---CTGGTACTGCAACAACCTACAGATTTCCAGGGTTCCTACAGTAGCACT 1692
 QY 475 Pro-----TyrGlyIysGlnGlyIysIleThrIleAsnIlePheSerThrAsp----- 489
 Db 1693 CTTACGCACTATGAGTATCAAGTACTTGGGAAATGACTTGGTGTATGATACCGCAAGC 1752
 QY 490 -----AspIysValIleThrValSerThrAlaIysGlnSerPheAsnProThrAla 506
 Db 1753 ACTCAAAAGCTAAGACAGCAGCACTTAGCTTGACATACAGCTTCCCAATCT 1812
 QY 507 GlnGlnGlnAlaProLeuValProAsnLeuLeuIleuIleuIleuPheIleAspValArgSer 526
 Db 1813 GAGGCTAAGAGCACTTATAGTCTTAATAGCTTGGGATCTTTTTCAGACATCCAAAGC 1872
 QY 527 PheGlnAsnPheIleGlyIleuGlyThrGlyIuIleProIysIysIysAspPheThrVal 546
 Db 1873 ATTCAAGGTGCATATAGAGAGAGCTTTGACTTTTGTTCAGATCAGAGCTTCTGGCT 1932
 QY 547 AlaGlyIleSerAsnValIleuHisArgSerGlyValArgIuAsnGlnArgIysPheArgHis 566
 Db 1933 GCGGAGATCGCCAAATTTCTTATGATTAAGATTAAGAAAGGCGAAACCGCAATACCGTCA 1992
 QY 567 ValSerGlyGlyAlaValAlaGlyIleAspThrArgPheProGlyIysAspThrIleuSer 586
 Db 1993 AAATCTGTGTATATGCTATGAGAGGTGACGCGCAAACTGTTGAAACTTAAATTAAGC 2052
 QY 587 LeuGlyPheAlaGlnIleuPheAlaArgAspIysAspIysPheMetAsnThrAspPheAla 606
 Db 2053 TTTGCCCTTTGCCCACTTTTGTGAGGATTAAGATTTCTTATGCGGCTAAATCATACT 2112
 QY 607 LysThrIysAlaGlySerLeuArgLeuGlnHisAspAlaSerLeuIysSerValValSer 626
 Db 2113 GATACCTATGACAGAGCTTCTATATCCACACATTAACAGATGTAGTGGGTCTATAGT 2172
 QY 627 IleLeuLeuGlyIuGlyIysIysLeuArgIuIleLeuLeuProIysValSerIysThrIleu 646
 Db 2173 TGTCTCTTAATTA-----CTTCTGGCTCTTGAAGTATATA 2211
 QY 647 ProCysSerPheIysGlyIleuSerIysIysIleThrAspHisArgMetIysThrGlu 666
 Db 2212 CCCCTCGTTTGAAGGACACTGCTTATAGCCACGTCAGTAATGATCTGAAGCAAG 2271
 QY 667 SerLeuProProProProIleuThrIleuSerThrAspHisIleThrIleuIysIysVal 686


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Db      2272 TATAGTCCATCTGAGGCG-----AAAGTCTCTGGGGAATATAGCT 2316
Qy      687 TTPALAGLYGLUENGLYTHRAVALAVALAGLUANTHSEGLYARGLYPHE--- 705
Db      2317 TTTAACATGATGTGGG-----GCTTCTTCTCATTTATCTCT 2355
Qy      706 -----PheGlnGluYrThrProPheValIleValGlnAlaValIleVal 720
Db      2356 GAATACCTGCATGTTTGTATACCTATGCTCCATACATCAATCAATGACCTATATA 2415
Qy      721 ATGGAATCCTCTCTCATGTTTAACTCGCATCTTTAGCACTTCCCTGACCTA 60
Db      2416 CCGACAGACAGCTTCTCGAGGAAGGATACAGAAAGATCTTTGATGACAGCAACCTC 2475
Qy      741 TTTAAATTCCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 120
Db      2476 TTTAAATTCCTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCTTCTGCT 120
Qy      758 GlnYrThrIleValIleValAlaMetTyrSerProAspValCysArgSerAspPro 777
Db      2533 TTTTCTTAATGATGATGATGATGATGATGATGATGATGATGATGATGATGATG 2592
Qy      778 ThrThrThrLeuLeuSerAsnGlnGlySerTyrPheThrIleGlySerAsnLeu 797
Db      2593 ACTACAGCACTTGTATACAGCGAGCGCTCTGGGAACTTATGCCAATATAGCA 2652
Qy      798 GlnAlaGlyIleValIleAlaSerGlyPheArgSerLeuGlyAlaIleGluLeu 817
Db      2653 CAGGCTTCTGCAAGTGTGCTGCAAGTCACTACGCTTCTCTCTCTCTCTCTCTCT 2712
Qy      818 GlnAsnPheGlyPheGluTyrPargIlySerSerTyrAsnValAspAlaGlySer 837
Db      2713 GGCAGTGTCTGTGTAAGTCTGATGATCTCTGATGATCTCTGATGATCTCTG 2772
Qy      838 LysIleLysPhe 841
Db      2773 AAGTTCATTC 2784

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Db

RESULT 9

US-10-312-273-34

Sequence 34, Application US/10312273

Publication No. US20040005667A1

GENERAL INFORMATION:

APPLICANT: CHIRON SPA

TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE

FILE REFERENCE: P025035WO

CURRENT APPLICATION NUMBER: US/10/312,273

PRIOR APPLICATION NUMBER: 0016363.4

PRIOR FILING DATE: 2000-07-03

PRIOR APPLICATION NUMBER: 0017047.2

PRIOR FILING DATE: 2000-07-11

PRIOR APPLICATION NUMBER: 0017983.8

PRIOR FILING DATE: 2000-07-21

PRIOR APPLICATION NUMBER: 0019368.0

PRIOR FILING DATE: 2000-08-07

PRIOR APPLICATION NUMBER: 0020440.4

PRIOR FILING DATE: 2000-08-18

PRIOR APPLICATION NUMBER: 0022583.9

PRIOR FILING DATE: 2000-09-14

PRIOR APPLICATION NUMBER: 0027549.5

PRIOR FILING DATE: 2000-11-10

PRIOR APPLICATION NUMBER: 0031706.5

PRIOR FILING DATE: 2000-12-22

NUMBER OF SEQ ID NOS: 664

SOFTWARE: SeqWin99, version 1.02

SEQ ID NO 34

LENGTH: 2787

TYPE: DNA

ORGANISM: Chlamydia pneumoniae

US-10-312-273-34

Alignment Scores:

Pred. No.: 4,396-131 Length: 2787

Score: 1379.50 Matches: 348

Percent Similarity: 49.53% Conservative: 124

Best Local Similarity: 36.52% Mismatches: 344

Query Match: 32.12% Indels: 137

DB: 12 Gaps: 22

US-09-830-446-27 (1-841) x US-10-312-273-34 (1-2787)

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Qy      1 MetLysIleProLeuArgPheLeuLeuIle-----SerLeuValProThrLeuSerMet 18
Db      1 ATGAATCCTCTCTCATGTTTAACTCGCATCTTTAGCACTTCCCTGACCTA 60
Qy      19 SerAsnLeuLeuGlyAlaIleThrGlu-----GluLeuSerAlaSerAsnSerPheAsp 37
Db      61 AATTCTCGCGTTTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120
Qy      38 GlnYrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThrThr 57
Db      121 GACACAGAACTACCTACCTCCACGCCAACAACAAATGCA-----GATGAACTATC 174
Qy      58 TyrValPheLysAspSerValIleGluAsnValProLysThrGlyIleThrGlnSer 77
Db      175 TATTAATCTTAACAGGAGATGCTCAATCAACCAATGCA---GATCTCCGACAGCTTAAC 231
Qy      78 ThrSerCysPheLysAsnAspAlaIleAlaGlyAspLeuAsnPheLeuGlyIlePhe 97
Db      232 GCTTCCTGCTTAAAGAA-----ACTACTGGAAATCTTCTTCCAAAGCCAGGCTAC 285
Qy      98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaIleGlySerGlu 117
Db      286 CAATTCCTCTCAAAATATCATGCG-----GAGCGCAACTGTACCTTACCAATACA 339
Qy      118 AlaIleAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerPro 137
Db      340 GCTGCATAATTAACCTTCTCTCTTTCAGGATCTCTCTTATTTGTCACTAATAAAC 396
Qy      138 AlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeu 157
Db      397 ---ACGAATGCTACCAAGAAACAGAGCATCAAGTCCACAGAGCTTGTCTATACG 453
Qy      158 AspAsnAspLysValLeuIleGlnAsnAsnPheSer----- 169
Db      454 TCGAATCTATAGTGTCTACTTGGCCAAACTTTTCTAATGACATGAGAGCGCCCTCCAA 513
Qy      169 ----- 169
Db      514 GGCAGCTATCAGTCTATCGCTAAACCCCACTAAGCTTGGCCAAACAAGCAAG 573
Qy      169 ----- 169
Db      574 CAAAAAGGGGGTCCCTCTATTCCAGGGAGGATTAACAATTACATTACGTTAAACTCA 633
Qy      169 ----- 169
Db      634 GCATCATTTTCTGAATAATCCGGCGGAACAATGCGGAGCATTTTACAGGAAGCTAGC 693
Qy      170 -----Thr 170
Db      694 AGTTTATTAGACAGCAACAAGCAATTAGCTTATTAACAATAGTGTGACCGCAACTCA 753
Qy      171 GlyAspGlyGlyAlaIleAsnGlyAsnGlySer-----LeuLysIle 184
Db      754 GCTACAGGGGGAGCAATTACTGTAGTATGATATGAGCCCAAAACAGCTCTTAACCTCA 813
Qy      185 AlaAsnAsnLysSerLeuSerPheIleGlyAsnSerSerSerThrArgGlyIleAlaIle 204
Db      814 TCAAGACAGCGGAACTGACTTATAGGAATACAGCAATTAAGTCTAGTGGGCGATT 873
Qy      205 HisThrLysAsnLeuThrLeuSerSerGlyIleGluThrLeuPheGlnGlyAsnThrAla 224
Db      874 TATAGTCAATCTAGTCTTCTTCTGAGGAGCACTACGCTTTTAAACAACACTCTGCT 933

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 LOCATION: (675001)..(690000)
 OTHER INFORMATION: n=a or c or g or t
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Alignment Scores:

Pred. No.: 1,72e-125 Length: 1230025
 Score: 1365.00 Matches: 329
 Percent Similarity: 51.04% Conservative: 161
 Best Local Similarity: 34.27% Mismatches: 320
 Query Match: 31.78% Indels: 151
 Gaps: 22

US-09-830-446-27 (1-841) x US-10-289-762-1 (1-1230025)

QY 1 MetlySileProLeuArpHeLeuLeuLeuSerLeuValProThrLeuSerMetSer 19
 DB 518200 ATGAATGCCAATTTTCCTGCTAGCTCTCTGCAATTCGCAATGTTTACTGTTCT 518141
 QY 20 AenLeuLeuGlyAlaAlaThrThrGluLeuSerAlaSerAsnSerPheLeuGlyThr 39
 DB 518140 TCCACTGTTTTCGCAACTCTGCAATATATAGCCCTCGATATAGCTTTGACGAAGT 518081
 QY 40 ThiserThrThrSerPheSerSerLeuThrSerAlaThrAspGlyThrAsnVal 59
 DB 518080 ACTAACACAGGACCTATACCTCTTAA-----AATACGACTCTGAAATAGACTTACT 518027
 QY 60 PheLyAspSerValValIleGluAsnValProLyThrGlyGluThrGlnSerThrSer 79
 DB 518026 CTGACAGGAGATATACTCTGAAAACCT-----GGGATTCGGACACTTTAACG 517976
 QY 80 -----GpPheLyAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyPhe 97
 DB 517975 AAGGCTGTTTTCGACACTACGGAATCT-----TTAAGCTTTCGGTAAAGGGTAC 517922
 QY 98 SerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGlu 117
 DB 517921 TCACTTCTTTTAAAT---ATMAAGTCTAGCTGAAGGGCAGANA-CTT---TCTGTT 517869

QY 118 AlaAlaAsnLyThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLeuSerPro 137
 DB 517868 ACACTGATMAAATCTGCTACAGAGATTTTCGAGTTACTTCTTAGCGGCCCA 517809
 QY 138 AlaSerThrValThr----- 142
 DB 517808 TCATCTGTAATCAACACCCTCAGAAAAGTGCAGTTAATGTGAGGGATCTTACA 517749
 QY 143 -----AengLy-Leu----- 145
 DB 517748 TTTGATACAAATGAACTATTATTATTAACAGATTACTGTAGAAAATGCGGACAT 517689
 QY 145 ----- 145
 DB 517688 TTCTACCAAAATCTTCTTTGAAAAACAGCAGGATTCATTTCTTTGAAGGAATTA 517629
 QY 145 ----- 145
 DB 517628 ATCGAGCGCAACAGGAAAAAGTGGGCTATTGTGCTACTGTAGATATTAC 517569
 QY 146 -----GlyAlaAla 148
 DB 517568 AATATATCGGCTCTACCTCTTCTGCAACATATTGCTAAGCTGACGATGACATAT 517509
 QY 148 eAsnValLySgLyAsnLeuSerLeuLeuAspAsnAspLyValLeuIleGlnAspAsnPh 168
 DB 517508 AATATGACACAGAAATCTGATCAATTAACAGGAATACGCTCTGTGATTTCTGAAAAATAG 517449
 QY 168 eSerThr-----GlyAspGlyGlyAlaAlaIleAsnValAlaGlySerLeuLySleAl 185
 DB 517448 TGTGACACGACCGACAGAAATGAGAGGCTCTTCTGAGATGCCGATTCACATATC 517389
 QY 185 AAsnAsnLySerLeuSerPheIleGlyAsnSerSerThrArgGlyAlaAlaIleH 205
 DB 517388 TGGGATACAGATGTAATCTTCTCAGAAACCAAGCTTACTATAGCGGAGCATTTA 517329
 QY 205 sThrLyAsnLeuThrLeuSerSer-----GlyGlyGluThrLeuPhe-GlnGlyA 222
 DB 517328 TGTATAGAAAGCTTACACTGCTCCGGGGGGGGGGGTATCTCTTTCTTAACATA 517269
 QY 222 snThrAlaProThrAlaAlaGlyLySgLyAlaAlaIleAlaIleAspSerGlyThrL 242
 DB 517268 TAGTCCAAAGTACCACTGACAGATATGTGAGCCATTTCTATATGCGACGTGAGAGT 517209
 QY 242 eSerLeSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAlaThr- 261
 DB 517208 GTAGCTTTCAGCAGAACAGGAGACATTACTTCAATGGAATGCCATTGTGCACTA 517149
 QY 262 -----GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaLySleThrAlaL 280
 DB 517148 CACCAAAATACGAAAAGAAATCTATTGACATGATGATCAACGAAGATTC 517089
 QY 280 euArgAlaAlaGlnGlyHisThrIleTyrrPheTyrrAspProIleThrValThrGlySert 300
 DB 517088 TACGGCAATATCTGGGATATGACATCTTTCTAGATCCATTAATCTCTAATACGGGCTG 517029
 QY 300 hrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnLySgLyTyT 320
 DB 517028 CGGATTCACAGATATCTTAATCTCAATAGCGTATGAGATATGATACAGATTATA 516969
 QY 320 hrGlyThrIleValPheSerGlyGlyLyLeuThrGluAlaGluAlaLySapGlyTyA 340
 DB 516968 GTGGGTGATGTTTCTGCTGTAAGAGCTCTGGAAGATGAAGCAAAAGTTGCAGACA 516909
 QY 340 snArgThrSerLyLeuLeuGlnAsnValAlaPheLyAsnGlyThrValValLeuLyBg 360
 DB 516908 ACCTCACTTCAACGCTGAAGACGCTGTACTTCACTGACGAAATATTAGACTTTAAC 516849
 QY 360 LyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLySleLeuMetA 380
 DB 516848 GTGGGTGACTCTGATACGAAGAGCTTTACTCAGACCGCGGTTCTCTGTATATTAGG 516789

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QY 380 spLeuGlyTherSerLeuValAlaAentThrGluSerIleGluLeuThraenLeuGluIleA 400
DB 516788 ATGCGGCGCAACGTTTAAAGAGATGACAGAGAGGACCTTAAACAGGCTTTTCATTC 516729
QY 400 enLeaSerLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 420
DB 516728 CTGTAAGACTCTTAAAGCGGAGGAGTAAAGAAAGTTGTAATGCTGCTTTCGACGAAGTAA 516669
QY 420 spLeaSerLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 440
DB 516668 ATGTAGCCCTTAAAGTGTGCGGATCTCTTTGATTAACCAAGGAATGCTTAAAGAAATC 516609
QY 440 lypheLeuGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 460
DB 516608 AGCACTTAAGAAAGAACTCAAGACTT---TCATTTGTGAGAGCTCTGCT---CTGGGTA 516555
QY 460 lvalIleSerLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 478
DB 516554 CTGCAACAACTACAGATGTTCCAGCGGTTCTTACAGTACAGACTCTTACGCACTATGGGT 516495
QY 478 yTGInGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 492
DB 516494 ATCAAGATCTTGGGAAATGACTGGGTTGATGATACCCGACAGACTCCAAAGACTTAA 516435
QY 492 yvalIleThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 512
DB 516434 CAGCGCATTAAGCTTGGCAATACCGGCTTCTTCAATCGATCGATCGATCGATCGATCGAT 516375
QY 512 euValProbenLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 532
DB 516374 TATGTTCTTAATAGCTTGGGATCTTGGGATCTTGGGATCTTGGGATCTTGGGATCTTGGGAT 516315
QY 532 luleuGlyThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 552
DB 516314 AAGAAGAGCTTGAAGCTTGTGATGATGAGAGCTTGTGATGAGAGCTTGTGATGAGAGCTTGT 516255
QY 552 alleuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 572
DB 516254 TCTTAAATTAAGTAAAGAAAGGGAAGAAAGGAAATACGCTAAATGCTTGGGATG 516195
QY 572 aIvalGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 592
DB 516194 CTATCGAGAGCTGAGCAAGCTTGTGATGATGAGAGCTTGTGATGAGAGCTTGTGATGAG 516135
QY 592 euPhaIleThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 612
DB 516134 TCTTGGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 516075
QY 612 erLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 632
DB 516074 CCTTGAATGCAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAA 516016
QY 632 lylGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 652
DB 516015 -----CTTCTGAGCTTGAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515976
QY 652 lylGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 672
DB 515975 GCGAGGCTTAAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515916
QY 672 rorProThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 692
DB 515915 AGGTG-----AAAGTCTTGGGGAATTAAGTCTTAAAGTAAAGTAAAGTAAAGTAA 515871
QY 692 lThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 706
DB 515870 GA-----GCTTCTTGAATCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515832
QY 706 heGInGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 726
DB 515831 TGTATCTTAAAGCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515772
QY 726 aIgluLeuGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 746

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DB 515771 CGAAGAAAGTACAGAGAGAGATCTTTGATGACAGCAAGCTTCAATTAATCTTGC 515712
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DB 515711 CTATAGGAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515655
QY 763 aIAlaMeThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 783
DB 515654 CTATATCTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515595
QY 783 erAenGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 803
DB 515594 TCAGCGGAGCTCTTGGGAACTTAAAGTAAAGTAAAGTAAAGTAAAGTAAAGTAAAG 515535
QY 803 lAlaSerGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 823
DB 515534 GTGAGGAGCTACATACGCTTCTCTCTATGTTGAAGTCTCGGCAAGTTGCTTGG 515475
QY 823 lUTPrAGlySerSerLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 841
DB 515474 AAGTGTGATCTTCAAGGATTAATGATGATCTTGGGGAATGATTCATTC 515419

RESULT 11
US-10-312-273-20
/ Sequence 20, Application US/10312273
/ Publication No. US20040005667A1
/ GENERAL INFORMATION:
/ APPLICANT: CHIRON SPA
/ TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
/ FILE REFERENCE: P025035WO
/ CURRENT APPLICATION NUMBER: US/10/312,273
/ PRIOR FILING DATE: 2002-12-20
/ PRIOR APPLICATION NUMBER: 0016363.4
/ PRIOR FILING DATE: 2000-07-03
/ PRIOR APPLICATION NUMBER: 0017047.2
/ PRIOR FILING DATE: 2000-07-11
/ PRIOR APPLICATION NUMBER: 0017983.8
/ PRIOR FILING DATE: 2000-07-21
/ PRIOR APPLICATION NUMBER: 0019368.0
/ PRIOR FILING DATE: 2000-08-07
/ PRIOR APPLICATION NUMBER: 0020440.4
/ PRIOR FILING DATE: 2000-08-18
/ PRIOR APPLICATION NUMBER: 0022583.9
/ PRIOR FILING DATE: 2000-09-14
/ PRIOR APPLICATION NUMBER: 0027549.5
/ PRIOR FILING DATE: 2000-11-10
/ PRIOR APPLICATION NUMBER: 0031706.5
/ PRIOR FILING DATE: 2000-12-22
/ NUMBER OF SEQ ID NOS: 664
/ SOFTWARE: SeqMan99, version 1.02
/ SEQ ID NO 20
/ LENGTH: 2241
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ US-10-312-273-20

Alignment Scores:
Pred. No.: 5,716-129 Length: 2241
Score: 1357.50 Matches: 330
Percent Similarity: 56.1% Conservative: 116
Best Local Similarity: 41.56% Mismatches: 270
Query Match: 31.61% Indels: 78
DB: 12 Gaps: 21

US-09-830-446-27 (1-841) x US-10-312-273-20 (1-2241)
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DB 16 TTTGAAATTAATCTTCAAGAAAGGAGGAGGATTAAGATTCGAGTCCCTTACATTC 75
QY 93 leuGlyGlyLeuThraenGlyLeuValIleLeuSerLeuAlaAlaThraIleGluIleA 112

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 Qy 133 PheLeuYSerProAlaSerThrValThrAsnGlyLeuGlyAlaIleAsnValIleGly 152
 Db 184 TTTATT----- 189
 Qy 153 AsnLeuSerLeuLeuAspAsnAspIleValIleLeuIleAsnAsnPheSerThrGlyAsp 172
 Db 190 -----GACATAAGCTCAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 231
 Qy 173 -----GlyGlyAlaIleAsnGlyAla-----GlySerLeuYsile 184
 Db 232 ATGTGAGAGAGGTCATC---TGTGCTTATTAACATGACATGACATGACATGACATGAC 288
 Qy 185 AlaAsnAsnLeuYSerLeuSerPheIleGlyAsnSerSerThrArgGlyGlyAlaIle 204
 Db 289 ACTGGAATCAGATGTTACTTTCAGCAACAATATCAGACAAACAGCGGAGAGAGCTATC 348
 Qy 205 HisThrIleAsnLeuThrLeuSerSerGlyGlyGlyThrLeuPhe----- 219
 Db 349 TATGTGAAGAAAGCTGAACTGGCTTCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 408
 Qy 220 GlnGlyAsnThrAlaProThrAlaAlaGlyGlyGlyAlaIleAlaIleAlaIleAspSer 239
 Db 409 AATGAGAGTACAGCTCTCT-----AAGGTGAGAGAGAGAGAGAGAGAGAGAGAGAG 456
 Qy 240 GlyThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGlyGlyAsnThrIleGly 259
 Db 457 GGGGATTTGAGTTTATCCCGCATGAGTGTGACATGTCTTTTGAAGAGATCAGTCACT 516
 Qy 260 AlaThr-----GlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaYsile 277
 Db 517 TCTACTACTCTGGAGAG---AATGAAGTATGATTCGACTTGAAGAGAGAGAGAGAGAG 573
 Qy 278 ThrAlaLeuArgAlaAlaGlnGlyHisThrIleTyPheTyAspProIleThrValThr 297
 Db 574 AAGCTTTCGCTTCGCTGCTGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 633
 Qy 298 GlySerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnYs 317
 Db 634 TCATCCACAACAGTTACAGATGCTTAAAGTTAATGAGAGCTCCGAGAGAGAGAGAGAG 693
 Qy 318 GlyTyThrGlyThrIleValPheSerGlyGlyGlyLeuThrGlyAlaGlyAlaYsAsp 337
 Db 694 CAATATACAGGAGAACATCTTCTACAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 753
 Qy 338 GlyTyAsnAspArgThrSerIleLeuGlnIleAsnValAlaPheTyAsnGlyThrValVal 357
 Db 754 TCTAAATAATCTTACTCGAAGCTTACAGCTGTACCTTTCAGAGAGAGAGAGAGAGAG 813
 Qy 358 LeuTyGlyAspValValLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLeu 377
 Db 814 TTAATAACATGAGTACCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 873
 Qy 378 IleMetAspLeuGlyThrSerLeu---ValAlaAsnThrGlySerIleGlyLeuThrAsn 396
 Db 874 GAAATGAG 927
 Qy 397 LeuGlnIleAsnIleAspSerLeuArgAsnGlyTyLeuIleLeuSerAlaIleAlaThr 416
 Db 928 TTGGTCATTAACATGATTTCTATAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 987
 Qy 417 AlaGlyTyAspIleArgIleAspArgProValValLeuAlaIleSerAspIleSerPhe 436
 Db 988 AGCTCAAAAG 1047
 Qy 437 TyArgIleAsnGlyPheLeuAsnGlyLeuAspIleSerTyAspGlyIleLeuGlyLeuAspAla 456
 Db 1048 TATGAAATCATAGTTTAAGAAATCTCAGTCTTACAGAC---ATCTTGAAGCTCAAAAGCT 1104

Qy 457 GlyTyAspIleValIleSerAla--AspSerArgSerIleAspAlaValGlnSerPro- 475
 Db 1105 TGTGGAAGTGTAAACAG 1164
 Qy 476 TyArgIleGlnGlyLeuTyr---ThrIleAsnThrSerThrAsp---AspIleYsAla 493
 Db 1165 TACGGCTTACAG 1224
 Qy 494 ThrValSerThrAlaIleGlnSerPheAsnProThrAlaGlnGlnAlaProLeuVal 513
 Db 1225 ACCTTCAACTGACTAAACCTGGCTATATCTTATATCCGAGAGAGAGAGAGAGAGAGAG 1284
 Qy 514 ProAsnLeuLeuTyrGlySerPheIleAspValArgSerPheGlnAsnPheIleGlyLeu 533
 Db 1285 CTTATACTTATGAGAAATGATATGATATGATGCTTCCATTAATATGAGAGAGCT 1344
 Qy 534 GlyThrGlnGlyAlaProTyGlyLeuArgPheTyrValAlaGlyIleSerAsnValLeu 553
 Db 1345 GCAAAAG 1404
 Qy 554 HisArgSerGlyArgGlyLeuAsnGlnArgIlePheArgHisValSerGlyValAlaVal 573
 Db 1405 CATAAAGATGATACAAAG 1464
 Qy 574 GlyAlaSerThrArgMetProGlyGlyAspThrLeuSerLeuGlyPheAlaGlnLeuPhe 593
 Db 1465 GAGAGAAACCTACATCTTGTTCAGATGAATGATCTTATGCTGATTTTGCAGAGCTTT 1524
 Qy 594 AlaArgAspIleAspTyPheMetAsnThrAsnPheAlaIleTyAlaGlySerLeu 613
 Db 1525 GGAAGAGATGAG 1584
 Qy 614 ArgLeuGlnIleAspAlaSerLeuTyrSerValIleSerIleLeuLeuGlyGlyGly 633
 Db 1585 TATTACAGCAACAAGAAACCTATATCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1626
 Qy 634 LeuArgGlnIleLeuLeuProTyValSerIleThrIleProCysSerPheTyGlyGln 653
 Db 1627 CTACGGCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1686
 Qy 654 LeuSerTyGlyHisThrAspHisArgMetLeuThrGlnSerLeuProProProPro 673
 Db 1687 CTTAGCTACACCCATACAGATACAGATGAGAAACCAAGATAT-----ACA 1731
 Qy 674 ThrLeuSerThrAspHisThrSerTyGlyGlyTyValTPrAlaGlyGlyLeuGlyThr 693
 Db 1732 ACATATCTTACTGTTAAAG 1791
 Qy 694 Arg-----ValAlaValGlnAsnThrSerGlyArgGlyPhePheGlnGlyTyThrPro 711
 Db 1792 AGAGCTCCGATTTGCTTATGATGAAAGTCT-----CATTTGAGAGAGAGAGAGAG 1842
 Qy 712 PheValIleValGlnAlaValTyAlaArgGlnAspSerPheValGlyLeuGlyAlaIle 731
 Db 1843 TTCAATGAATGAG 1902
 Qy 732 SerArgAspPheSerAspSerHisLeuTyArgIleAsnIleIleProLeuGlyIleYsLeu 751
 Db 1903 GCTGCTGAATTTGAG 1962
 Qy 752 GlyTyAspArg-----PheAlaGlnGlnTyTyHisValValAlaMetTySerProAsp 769
 Db 1963 GATTAAGAAATGAG 2022
 Qy 770 ValCysArgSerAspProIleCysThrThrThrLeuLeuSerAsnGlnGlySerTyIle 789
 Db 2023 CTTGTTCTTATTAACCCCGAG 2082
 Qy 790 ThrIleGlySerAsnLeuAlaArgIleAlaGlyIleValGlnAlaSerGlyPheArgSer 809
 Db 2083 ACCTTGGATGAGAAATTTGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 2142

QY 810 LeuGLyAlAlAlaLeuPheGLyAsnPhesGLyTrpArgGLySerSerArg 839
 DB 2143 TTTAACTTATCAATTCAGGCTTACGCAATTTCTTGAATTCGCTGATCTCGC 2202
 QY 830 SerTyrAsnValAspAlaGLySerGLyIleLysPhe 841
 DB 2203 AATTACAAATGTAGACTTAGAGCAAAATACCAATTC 2238
 RESULT 12
 US-10-312-273-154
 / Sequence 154, Application US/10312273
 / Publication No. US20040005667A1
 / GENERAL INFORMATION:
 / APPLICANT: CHIRON SPA
 / TITLE OF INVENTION: IMMUNISATION AGAINST CHLAMYDIA PNEUMONIAE
 / FILE REFERENCE: P025035MO
 / CURRENT APPLICATION NUMBER: US/10/312.273
 / CURRENT FILING DATE: 2002-12-20
 / PRIOR APPLICATION NUMBER: 0016363.4
 / PRIOR FILING DATE: 2000-07-03
 / PRIOR APPLICATION NUMBER: 0017047.2
 / PRIOR FILING DATE: 2000-07-11
 / PRIOR APPLICATION NUMBER: 0017983.8
 / PRIOR FILING DATE: 2000-07-21
 / PRIOR APPLICATION NUMBER: 0019368.0
 / PRIOR FILING DATE: 2000-08-07
 / PRIOR APPLICATION NUMBER: 0020440.4
 / PRIOR FILING DATE: 2000-08-18
 / PRIOR APPLICATION NUMBER: 0022583.9
 / PRIOR FILING DATE: 2000-09-14
 / PRIOR APPLICATION NUMBER: 0027549.5
 / PRIOR FILING DATE: 2000-11-10
 / PRIOR APPLICATION NUMBER: 0031706.5
 / PRIOR FILING DATE: 2000-12-22
 / NUMBER OF SEQ ID NOS: 664
 / SOFTWARE: SeqMan9, version 1.02
 / SEQ ID NO 154
 / LENGTH: 2811
 / TYPE: DNA
 / ORGANISM: Chlamydia pneumoniae
 US-10-312-273-154
 Alignment Scores:
 Pred. No.: 1,486-126 Length: 2811
 Score: 1335.50 Matches: 311
 Percent Similarity: 49.26% Conservative: 157
 Best Local Similarity: 32.74% Mismatches: 359
 Query Match: 31.09% Indels: 123
 Gaps: 14
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 DB 1 AATGAATCTCTGCTCTCTGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 60
 QY 21 LeuLeuGLyAlAlAlaThrArgLysIleLeuSerAlaSerAsnSerPheAspGLyThrThr 40
 DB 61 ATAGTCGGCGAGAGGTGACCTTAGAT--AGCAGCAATATATGCTATATGATGATCTAAC 117
 QY 41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGLyThrAsnTyrValPhe 60
 DB 118 GGAACCTACCTTACCGCTCTTTCACCTACGAGCGCTCTCGACGAACTACCTATTCCTTA 177
 QY 61 LysAspSerValValIleGluAsnValProLysThrGLyLysIleThrGlnSerThrSerCys 80
 DB 178 CTTTCCGACTATCTCTTCAAAATGCGAGGGCTTAGAAATCCCTTAGCCTCAGGATGC 237
 QY 81 PheLysAsnAspAlaAlaIleGLyAspLeuAsnPheLeuGLyGLyLysPheSerPheThr 100
 DB 238 TTCTTGAAGAA-----CGGGGGCGAGATCTTACTTCCAAAGAAATCAACATGCACTGAAG 291
 QY 101 PheSerAsnIleAspAlaThrThrAlaSerGLyAlaAlaIleGLySerGluAlaIleAsn 120

DB 292 TTTCATTTATCAATCGGGGCTCTACGCTGGAACGTAGCCAGTACCTCAGCAGCAGAT 351
 QY 121 LysThrValThrLeuSerGLyPheSerAlaLeuSerPheLeuLysSerProAlaSerThr 140
 DB 352 AAGAAATCTCTCTTATATATTTTCTTGAATCTCTTATATATCTTGTCTCTCTCTCT 411
 QY 141 ValThr---AsnGLyLeuGLyAlaIleAsnValLysGLyAsnLeuSerLeuAspAsn 159
 DB 412 CTCTCTCTACCTGAGCAATGCTTTAAATCTGTGGGAATATATCTTACTGCAAT 471
 QY 160 AspLysValLeuIleGlnAspAsnPheSerThrGLyAspGLyAlaIleAsn----- 177
 DB 472 TCCCAATATATATTACTCAGAACTCTCTCAGATACGCGGGTGTATCAATACGAA 531
 QY 177 ----- 177
 DB 532 AACTTCTTATATACAGGACATCTCAGTTGGAGCTTTTCGAGAAACCAAGCCTTCACA 591
 QY 178 -----CysAlaGLySerLeuLysIleAlaAsn----- 186
 DB 592 GGGAGCAAGGGGTGTAGTTAGCTACAGAACTATACATCTACAGAACAGCCCTGGG 651
 QY 186 ----- 186
 DB 652 ATAGTTTCTCTCTCAAAACCTAGCGAAGAGATCTGGGGTCTCTGTACAGACTGAC 711
 QY 186 ----- 186
 DB 712 AACTGTTCATTACAGATTAATTCAAGTATCTTTCAGCGCAATAGTCTTGGAGACC 771
 QY 186 ----- 186
 DB 772 GCTCAAGCTCAGGGCGGGCTATTTGTCACATGACAGATTAACAGTACTTACT 831
 QY 187 ---AsnLysSerLeuSerPheIleGlnAsnSerSerThrArgGLyAlaIleAsn 205
 DB 832 GGGAAACAAACCTCTCTTCAAAATATACGATTCAGATGCAATATGCGGAGCAGCTCT 891
 QY 206 ThrLysAsnLeuThrLeuSerSerGLyGLyLysIleThrLeuPheGlnLysThrAlaPro 225
 DB 892 GGACTCAAGTCAAGATATTCCTCGAGGCTCTACTCTTTCAAAGTATATCTCAGGA 951
 QY 226 ThrAlaAlaGLyLys-----GlyGLyAlaIleAlaIleAspSerGLyThrLeuSer 243
 DB 952 AGTAGCGCGGTCAGGAGAGAGAGAGATCAATATATGCAATCTGCTGAGAACTCGCT 1011
 QY 244 IleSerGLyAspSerGLyAspIleIlePheGlnLysThrIleGLyAlaThrGLyThr 263
 DB 1012 CTCTGCTACTCTTGGAGATATTAACCTTCATTAACAACCAAGTACCAAGCAGACACA 1071
 QY 264 ValSerHisSerAlaIleAspLeuGLyThrSerAlaLysIleThrAlaLeuArgAlaIle 283
 DB 1072 AGTACAGAAACGCAATATATATCAATTGATCCGCTAAAGTCAATCGATGAGCTGCT 1131
 QY 284 GlnGlnHisLeuThrIleTyrPheThrAspProIleThrValThrGlySerHisSerValAla 303
 DB 1132 ACGGGCAATCTATCTATTTATATGATCCATCAACATCCAGAAACCCAGCTTCTACC 1191
 QY 304 AspAlaLeuAsnIleAsnSerProAspThrGLyAspAsnLysGLyLysThrGLyThrIle 323
 DB 1192 GACACATTGAATTAATTAACATGAGATGCGAACAGTGAAGATGGGGGTGCAAT 1251
 QY 324 ValPheSerGLyGLyLysLeuThrGLyAlaGLyAlaLysAspGLyLysAsnArgThrSer 343
 DB 1252 GTCCTTTCTCGAAGAAAGCTTTCCTTACAGAAAGCAATGCTGCAACCTCACTCT 1311
 QY 344 LysLeuLeuGlnAsnValAlaPheLysAsnGLyThrValValLeuLysGLyAspValVal 363
 DB 1312 ACTATTCGACAACTGCAATATTAGCGCGGGAGATCTTGTACTCTGTATGAGAGTCAAC 1371
 QY 364 LeuSerAlaAsnGLyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGLyThr 383

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Db      1372 GTAACCTTCAGAGATCTGACCAAGTCCGAGATCCCGCATCTTAATGATGGGGGACT 1431
Qy      384 SerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGluIleAsnIleAspSer 403
Db      1432 ACACTTAGTGTAAAGAGCAAAATCTTCGCTTAATGCGCTTAAGCAATATCTCTCTCT 1491
Qy      404 LeuArgAsnGlyLysLeuIleLeuSerAlaAlaThrAlaGlnLysAspIleArgIle 423
Db      1492 TTAGATGGAACCAACAGGAGAGCTTTAAAGAACGAGCTGCAAGATTAATAATTCAGCCCA 1551
Qy      424 AspArgProValValLeuAlaIleSerAspGluSerPheTyrGlnAsnGlyPheLeuAsn 443
Db      1552 TCGGGAACCATTCGCTTATTTGACACGGAAGGCTCATCTTAATGAGATCATTAATTAATA 1611
Qy      444 GluAspHisLeuSerTyrAspGlyLysLeuGluLeu---AspAlaGlyLysAspIleValIle 462
Db      1612 AGTGTAGTACTATCTCT---CTTCTTGAACCTTACACCGGAGAGACCAAGCAAGAT 1668
Qy      463 SerAlaAspSerArgSerIleAspAlaValGlnSerPro-----TyrGlyTyrGln 479
Db      1669 ACTGTGGAGAGCTCTTCTACCGTCACTCTTCAAGAACCTGAAACCACTACGGGATTCACA 1728
Qy      480 GlyLysTyrThrIleAsnTyr-----SerThrAspAspLysLysValaThrValSerTyr 497
Db      1729 GGAAACTGGCAGATGTGCTTGGGCAAAATGCAACATCTCTCAAAAATAGGAAGCATCACTGG 1788
Qy      498 AlaLysGlnSerPheAsnProThrAlaGlnGlnGluAlaProLeuValProAsnLeuLeu 517
Db      1789 ACCCGTACAGATACATCTCTAGTCTCTGAGAGAAAAGTAATCTCTCTTAATAGCTTA 1848
Qy      518 TTPGlySerPheIleAspValArgSerPheGlnAsnPheIleGluLeuGlyThrGluGly 537
Db      1849 TGGGGAATCTTATAGATATACCGTCAATCACTCACTCACTCACTCACTCACTCACTCACT 1908
Qy      538 AlaProTyrGluLysArgPheTyrValAlaGlyIleSerAsnValIleuHisArgSerGly 557
Db      1909 GAGCTTTTGAAGCGTACGCTATGCGCTTCAAGAAATTCGCAATTTCTCTATAGAGATCT 1968
Qy      558 ArgGluAsnGlnArgLysPheArgHisValSerGlyAlaValAlaGlyLysSerThr 577
Db      1969 ATGCCACCGGCGCATGCTTCCGCAATATCAAGCGGGGTTATGCACTAGAGATCAACAGCA 2028
Qy      578 ArgMetProGlyLysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db      2029 ACAACCTCCGCGAGATCAAGCTACTTTGCTTCTGCAAGCTCTTCTGAGAGATCC 2088
Qy      598 AspTyrPheMetAsnThrAsnPheAlaLysThrTyrAlaGlySerLeuArgLeuGlnHis 617
Db      2089 AATCATATATACAGTAAAGAACCAAGAGATTAATTAAGGCTCTTGTATATTCACCAT 2148
Qy      618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGluGlyLysLeuArgGluIle 637
Db      2149 ACAAGAGGCTCTTCAACATCCGCAATTTCTCTGAGGAAAGCAACCGAGCTCCCTGG 2208
Qy      638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyLysLeuSerTyrGly 657
Db      2209 GTGCTCTCGAGATCTCCAGATCATCTTATCTGATGAGTAAATTCAGTATCTTC 2268
Qy      658 HisThrAspHisLeuArgLysThrGluSerLeuProProProProThrLeuSerThr 677
Db      2269 CATACAGACCAACCAATGAAG-----ACATATATATACC 2301
Qy      678 AspHisLeuTh-----SerTyrGlyLysTyrValTTPAlaGlyLysLeuGlyThr 693
Db      2302 GATTAATCTATCATCAAGGCTCTTGAAGAAACGATGCTCTGTCGCAATCTTGAAGCT 2361
Qy      694 ArgValAlaValAlaGluAsnThrSerGlyArgGlyPhePheGlnGluTyrThrProPheVal 713
Db      2362 AGCGTGCCTTTGTT---ATTTCGTCGTAATCTCTGAAGAAATTCAGACCTTTTGTCT 2418
Qy      714 LysValGlnAlaValTyrAlaArgIleAspSerPheValGluLeuGlyAlaIleSerArg 733
Db      2419 AAAGTACAGTATATCTATGCGCATGCAAGACTTCTACAGCGCTCATGCTGAAGAGCC 2478

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Qy      724 AspPheSerAspSerHisLeuTyrAsnLeuAlaIleProLeuGlyLysLeuGlyLys 753
Db      2479 GCTTTCATTAAGAGAGACTTATCAAGCTAGAGATCTCTATAGCGTCACTTCAAGAA 2538
Qy      754 -----ArgPheAlaGluGlnTyrThrIleValAlaAlaMetTyrSerProAspValCys 771
Db      2539 GACTCAAAATATGAAAGAAAGGAACCTTACATGATCTTATAGTATATATCTGATCTTAC 2598
Qy      772 ArgSerAsnProLysCysThrThrThrLeuLeuSerAsnGlnGlySerTyrLysThrLys 791
Db      2599 CGACCAATCTCTTAATGCAAACTCCCTTAATAGCTACGATGCTACTGATGAGTGGCTTAT 2658
Qy      792 GlySerAsnLeuAlaArgGlnAlaGlyLysLeuAlaGlnAlaSerGlyPheArgSerLeuGly 811
Db      2659 GGTACCAACCTGCGACGACAGACAGCTTTTCTGTGCTGCGAACCATTTCCAGTGAAC 2718
Qy      812 AlaAlaAlaGluLeuPheGlyAsnPheGlyPheGluTyrPargLysSerArgSerTyr 831
Db      2719 CCCCAATGGAATCTTGGTCAATTCGCTTTGAAAGTACGAAGTCTTCAAGAAATATAT 2778
Qy      832 AsnValAspAlaGlySerLysIleLysPhe 841
Db      2779 AATACAAACTAGGCTCTTAAGTTTGTTC 2808

RESULT 13
US-09-452-380-1
/ Sequence 1, Application US/09452380
/ Patent No. US2002009340A1
/ GENERAL INFORMATION:
/ APPLICANT: MURDIN, Andrew D.
/ APPLICANT: KUMEN, Raymond P.
/ APPLICANT: WANG, Joe
/ APPLICANT: DURN, Pamela
/ TITLE OF INVENTION: CHLAMYDIA ANTIGENS AND CORRESPONDING DNA FRAGMENTS AND
/ FILE REFERENCE: US02931/0216
/ CURRENT APPLICATION NUMBER: US/09/452,380
/ PRIOR FILING DATE: 1999-12-01
/ PRIOR APPLICATION NUMBER: US 60/132,272
/ PRIOR FILING DATE: 1999-05-03
/ PRIOR APPLICATION NUMBER: US 60/113,439
/ PRIOR FILING DATE: 1998-12-01
/ NUMBER OF SEQ ID NOS: 6
/ SOFTWARE: PatentIn Ver. 2.0
/ SEQ ID NO 1
/ LENGTH: 3050
/ TYPE: DNA
/ ORGANISM: Chlamydia pneumoniae
/ FEATURES:
/ NAME/KEY: CDS
/ LOCATION: (101)..(2908)
/ US-09-452-380-1

Alignment Scores:
Pred. No.: 1,68e-126 Length: 3050
Score: 1335.50 Matches: 311
Percent Similarity: 49.26% Conservative: 157
Best Local Similarity: 32.74% Mismatches: 359
Query Match: 31.09% Indels: 123
DB: 9 Gaps: 14

US-09-830-446-27 (1-841) x US-09-452-380-1 (1-3050)
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Qy      21 LeuLeuGlyAlaAlaThrThrGluGluLeuSerAlaSerAsnSerPheAspGlyThrThr 40
Db      161 ATAGTCGGGCGAGAGTACCTTAGAT---AGCAGCAATTAAGCTATAGATGATCTTAAC 217
Qy      41 SerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyrValPhe 60

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Db 218 GGAAGTACCTTCAAGGCTTTTCCACTACGACGCTGCTCAGAAATCTACTTCTTCA 277
Qy 61 LysAspSerValValIleGluAsnValProLysThrGlyLysThrGlnSerThrSerCys 80
Db 278 CTTCCGACCTATCTCTTCAAAATGCGAGGCGCTTAGAAATCCCTTAGCTCAGATGC 337
Qy 81 PheLysAsnAspAlaAlaAlaGlyAspLeuAsnPheLeuGlyGlyGlyPheSerPheThr 100
Db 338 TTCTCTAGAA-----GCGGCGCGGATCTTACTTCCAGGAAATCAACATGACGAGAG 391
Qy 101 PheSerAsnIleAspAlaThrThrAlaSerGlyAlaAlaIleGlySerGluAlaAlaAsn 120
Db 392 TTTCGATTATCAATGCGGCTCTAGCGCTGGAACCTGACCACTGACCTCAGACGACAGAT 451
Qy 121 LysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProLysThr 140
Db 452 AGAATCTCTCTTAAATGATTTTCTAGACTCTCTATTTATCTCTTGTCTCTCTTCTT 511
Qy 141 ValThr---AsnGlyLeuGlyAlaIleAsnValLysGlyAsnLeuSerLeuAspAsn 159
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Qy 160 AspLysValLeuIleGlnAspAsnPheSerThrGlyAspGlyAlaAlaAsn----- 177
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Qy 177 ----- 177
Db 632 AACTTCTTATTATCAGGACATCTCAAGTTGCGAGCTTTGAGAAACCAAGCTTCACA 691
Qy 178 -----CysAlaGlySerLeuLysIleAlaAsn----- 186
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Qy 186 ----- 186
Db 752 ATAGTTCTTCTCTCAAAACCTAGCGAAAGATCTGCGGTCTCTGTACAGACTGAC 811
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Db 812 AACTGTTGATTAACAGATTAATTCAAGTATCTTTGACGCGCAATAGTCTTGGAAACC 871
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Db 872 GCTCAAGCTCAAGGCGGCGCTATTTGTTGACACTACAGACATAAAACAGTACTTACT 931
Qy 187 ---AsnLysSerLeuSerPheIleGlyAsnSerSerThrArgGlyAlaIleHis 205
Db 932 GCGAACAATAACCTCTCTTCACAATAATATACAGACTTACATATGCGGAGCCATCTCT 991
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Db 992 GGACTCAAGGCTCAATATTTCCGAGGCTCTACTCTATTTCAAAAGTAAATATATCTGGA 1051
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Db 1052 AGTAAAGCGCGCTCAGAGAGAGAGAGAGATCAATATACATCTGCTGGGAACTCGCT 1111
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Qy 284 GlnGlyHisThrIleThrPheThrAspProIleThrValThrGlySerThrSerValAla 303
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Qy 364 LeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThr 383
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Qy 384 SerLeuValAlaAsnThrGlnSerIleGlyLeuThrAsnLeuGlnLysAsnIleAspSer 403
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Db 1652 TCGGAACGATTCGCTTATTTGACAGGAGGCTCATTTATGAGATCATTAATTAATAA 1711
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Db 1769 ACTCTGAGAGCTCTTCTTCAACCTGACTCTTCAAGAACCTGAACCCAGCTACGAGTACA 1828
Qy 480 GlyLysTrpThrIleAsnTrp-----SerThrAspAspLysLysAlaThrValSerTrp 497
Db 1829 GGAACCTGCAAGTTGCTTGGGCAATGCACATCTCTCAAAATATAGAACATCAACTGG 1888
Qy 498 AlaLysGlnSerPheAsnProThrAlaGlnGluAlaProLeuValProAsnLeuLeu 517
Db 1889 ACCGTAACAGATACATTCCTAGTCTCTGAGAGAAAGTAAATCTCTCTTAATTAAGCTTA 1948
Qy 518 TrpGlySerPheIleAspValArgSerPheGlnAsnPheIleGlyLeuGlyThrGlyGly 537
Db 1949 TGGGAAACTTATATAGATATAGCTGATCAATCAAGCTTATAGAAACCAAGTCCAGTGG 2008
Qy 538 AlaProTyrGlyLysArgPheTrpValAlaGlyIleSerAsnValLeuHisArgSerGly 557
Db 2009 GAGCTTTTGAAGCGTATGAGCTATGCTTTCAGGAATTCGCAATTTCTTATATAGAGATTCT 2068
Qy 558 ArgGluAsnGlnArgLysPheArgHisValSerGlyAlaValAlaGlyAlaSerThr 577
Db 2069 ATGCCACCGGCGATGCTTTCGCAATATCAGGCGGAGTTATGACCTAGGAGATCACAGCA 2128
Qy 578 ArgMetProGlyLysAspThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLys 597
Db 2129 ACAACCTCTCGCGAGATACAGCTTACTTTTGGCTTCTGACAGCTTTTGTATAGATTCG 2188
Qy 598 AspTyrPheMetAsnThrAsnPheAlaLysTrpTyrAlaGlySerLeuArgLeuGlnHis 617
Db 2189 AATCATATTAACAGTAAAGAACCGAGATATCTTACGCTCTTGTATTTCCACAT 2248
Qy 618 AspAlaSerLeuTyrSerValValSerIleLeuLeuGlyGlyGlyLysLeuArgGluIle 637
Db 2249 ACAAGAGGCTCTTGCACATTCGCAATTCCTCTGCGGAAAGCAACCGAGCTCCCTGG 2308
Qy 638 LeuLeuProTyrValSerLysThrLeuProCysSerPheTyrGlyGlnLeuSerTyrGly 657
Db 2309 GTCCTCTCGAGATCTCCAGATCATCTCTTATGCTTATGATGCTTAATTCAGTTATTC 2368
Qy 658 HisThrAspHisArgLysLysThrGlnSerLeuProProProProThrLeuSerThr 677
Db 2369 CATACAGAACACACATGAAG-----ACATATTATTAACC 2401
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Qy	678	AspIsthr-----SetrpolyltyrValtPralaglLleuLgltThr	693
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Db	2402	GATAACTCATCAACAGGGTCTTGGAGAAACAGCTCTGTGCGAGACTTGGAGCT	2461
		:::	
Qy	694	ArgValalavalGluantThrSerLylArgqlYphehnglnlYrThrProPheVal	713
		:::	
Db	2462	AGCCTCGCTTGTGTT---ATTTCGGTTCGGATCTTCGAAAAGAGTGGAACTTTTGTC	2518
		:::	
Qy	714	LysValglinalValtYrAlArgqlnApsSerPheValGluLeuGlYAlaIleSerArg	733
		:::	
Db	2519	AAATTAACGATATCTATTCGCGATACGAGAACTTTCAGAGCTCATGCGAAGAGAGC	2578
		:::	
Qy	734	AspPheSerApsSerHlslLeuYrApsLeuAlaIleProLeuGlYlLeYLeuGlulYs	753
		:::	
Db	2579	GCTTTCATATMAACGAGCTTATCAACCTAGAGATTCTTAAGCGGTCACTTGAAAGA	2638
		:::	
Qy	754	-----ArpPhealaglInlYrThlsvAlalAlaMetYrSerProApsValCys	771
		:::	
Db	2639	GACTCAAAATGAGAAAGGAACTTACATCTTACTTATGTAATATCTGAGCTTAC	2698
		:::	
Qy	772	ArgSerAnProLysCyethrThrThrLeuLeuSerApsnglnYSerTlYrThlYs	791
		:::	
Db	2699	CGAGCGACATCTTAATGTCAAACTTCCCTAATAGCTAGAGTCACTGATGGCTAT	2758
		:::	
Qy	792	GlySerLeuLeuAlaArgGlinalglYlLeValGlnAlaSerGlYpheaYSerleuGlY	811
		:::	
Db	2759	GTATCAACCTCGACACAGAGTTTTCGTGTCGTGGAAACATTTCCAAAGTAAAC	2818
		:::	
Qy	812	AlaIlaIlaGlueupheglYAsnPhedlYphegluTPrAgglYSerSerArgSerYr	831
		:::	
Db	2819	CCCCACATGGAATCTTCGGTCAATGCGCTTTGAAGTACGAAGTCTTCCAGAAATTAT	2878
		:::	
Qy	832	AsnValApsAlaglYSerlYsIleLeYpHe	841
		:::	
Db	2879	AATACAAACTTAGGCTCTAAAGTTTGTGTTTC	2908

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US-10-324-129-1
: Sequence 1, Application US/10324129
: Publication No. US20030157124A1
: GENERAL INFORMATION:
: APPLICANT: Murdin et al.
: TITLE OF INVENTION: Chlamydia antigens and corresponding DNA fragments and uses thereof
: FILE REFERENCE: 77813-4
: CURRENT APPLICATION NUMBER: US/10/324,129
: CURRENT FILING DATE: 2002-12-20
: PRIOR APPLICATION NUMBER: US 60/113,439
: PRIOR FILING DATE: 1998-12-01
: PRIOR APPLICATION NUMBER: US 60/132,272
: PRIOR FILING DATE: 1999-05-03
: NUMBER OF SEQ ID NOS: 6
: SOFTWARE: PatentIn Ver. 2.0
: SEQ ID NO 1
: LENGTH: 3050
: TYPE: DNA
: ORGANISM: Chlamydia pneumoniae
: FEATURES:
: NAME/KEY: CDS
: LOCATION: (101)..(2908)
: US-10-324-129-1

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Alignment Scores:	
Pred. No.:	1,686-126
Score:	1335, 50
Percent Similarity:	43,284
Best Local Similarity:	32,774
Query Match:	31,094
DB:	13
Gaps:	14
Length:	3050
Matches:	311
Conservative:	157
Mismatches:	359
Indels:	123

US-09-830-446-27 (1-841) x US-10-324-129-1 (1-3050)
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1 MetLysIleProLeuArgPheLeuLeuIleSerLeuValProThrLeuSerMetSerAsn 20

[illegible]

Db 1172 AGTACAGAAAGCGAATTAATCATGATACCGTAAGTCATCGATACGAGCTGCT 1231
 QY 284 GINGLYHIEthRIeThyPheTyraAPProIeThValThrgIySeThrSerValAla 303
 Db 1232 AGGGGCAATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCTATCT 1291
 QY 304 AApAlaLeuAenIleAenSerProAerThrgIyAspAenIyIyThrgIyThrgIy 323
 Db 1292 GACACATTGAACCTTAATCTTAAGAGATGCGAACGATGAGATGAGATGAGATGAGAT 1351
 QY 324 ValPheSerGIyGIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIy 343
 Db 1352 GCTTTTTCGAGAAAGAGCTTTCCTCAAGAAAGAGCTTTCCTCAAGAGCTTTCCT 1411
 QY 344 LyLeuLeuGIyIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIy 363
 Db 1412 ACTATCGACACCTGACATTAAGCGGGGAGATCTTGTATCTGATGAGATGAGATGAG 1471
 QY 364 LeuSerAlaAenIyPheSerGIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIyIy 383
 Db 1472 GATACCTTCAAGATGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 1531
 QY 384 SerLeuValAlaAenThrgIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIyIy 403
 Db 1532 ACACCTAGTGTAAAGAGCGAATCTTTCCTTAATGCTTACGATTAATCTTCTCTCT 1591
 QY 404 LeuArgAenGIyIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIy 423
 Db 1592 TTATGATGACCAACAGGAGCTTTTAAAGAGCTGATTAATTAATTAATTAATTAAT 1651
 QY 424 AspArgProValAlaLeuAlaIleSerAspGIyIyLeuThrgIyIyLeuThrgIyIy 443
 Db 1652 TCGGAAACATTCGCTTATGACAGGAAAGGCTTATGATGATGATGATGATGATGAT 1711
 QY 444 GIyAspHisSerTyraPheGIyIyIyLeuThrgIyIyLeuThrgIyIyLeuThrgIy 462
 Db 1712 AGTGTAGTACCTATCTCTCTTGAATTAATCAAGCGAGAGAGAGAGAGAGAGAG 1768
 QY 463 SerAlaAenSerArgSerIleAenAlaValGIyIyLeuThrgIyIyLeuThrgIyIy 479
 Db 1769 ACTCTGGAGAGCTTTTCTACCTGACCTTCAAGAGAGAGAGAGAGAGAGAGAGAG 1828
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 QY 518 TTGGLySerPheIleAenValAlaArgSerPheGIyIyIyLeuThrgIyIyIyIyIy 537
 Db 1949 TGGGAAACCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2008
 QY 538 AlaIy 557
 Db 2009 GAGCCTTTGAGAGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2068
 QY 558 ArgGIy 577
 Db 2069 ATGCCACACCGGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2128
 QY 578 ArgMetProGIy 597
 Db 2129 ACAATCTCTGCGAGATGATGATGATGATGATGATGATGATGATGATGATGATGAT 2188
 QY 598 AspTyraPheMetAenThrgIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 617
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QY 638 LeuLeuProTyraValSerIyThrgIyIyLeuProCySerPheTyraGIyIyIyLeuSerTyraGIy 657
 Db 2309 GTCCTCTCGAGATCTCCAGATCAATCTCTTATCTGATGATGATGATGATGATGATGAT 2368
 QY 658 HisThraPheIy 677
 Db 2369 CATACAGACCAACCATGAAG-----ACATTAATTAATTAATTAATTAATTAATTAAT 2401
 QY 678 AspHisIleTh-----SerTyrGIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 693
 Db 2402 GATTAATCTATCATCAAGGCTTTCGAGAAAGATGCTTTCGAGAAAGATGCTTTCGAG 2461
 QY 694 ArgValAlaIy 713
 Db 2462 AGCCTGCTTTTGT---ATTTCGCTCCGATCTTTCGAGAAAGATGCTTTCGAGAAAG 2518
 QY 714 LyValGIy 733
 Db 2519 AAAGTACATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2578
 QY 734 AspPheSerAspSerHisLeuTyraIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 753
 Db 2579 GCTTCAATTAAGAGGCTTATCAAGATGATGATGATGATGATGATGATGATGATGAT 2638
 QY 754 -----ArgPheAlaGIy 771
 Db 2639 GACTCAAAATCAAGAAAGGAACTTTCGATCTTATGATGATGATGATGATGATGATGAT 2698
 QY 772 ArgSerAenProIy 791
 Db 2699 CGACGCAATCTTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2758
 QY 792 GIySerAenLeuAlaArgGIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIyIy 811
 Db 2759 GGTACCAACCTGCGAGAGAGGTTTCTGTCGTCGCGAGAGAGAGAGAGAGAGAGAG 2818
 QY 812 AlaAlaIy 831
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RESULT 15
 US-09-738-269-56
 / Sequence 56, Application US/09738269
 / Publication No. US2003018548A1
 / GENERAL INFORMATION:
 / APPLICANT: JOHNSTON, STEPHEN A.
 / APPLICANT: STECKE-HALE, KATHERINE
 / APPLICANT: SYKES, KATHRYN F.
 / APPLICANT: KALTENBOECK, BERNHARD
 / TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR VACCINATION COMPRISING
 / TITLE OF INVENTION: NUCLEIC ACID AND/OR POLYPEPTIDE SEQUENCES OF
 / TITLE OF INVENTION: CHLAMYDIA PSITTAZI
 / FILE REFERENCE: US/09-738,269
 / CURRENT APPLICATION NUMBER: US/09/738,269
 / NUMBER OF SEQ ID NOS: 61
 / SOFTWARE: PatentIn Ver. 2.1
 / SEQ ID NO 56
 / LENGTH: 2781
 / TYPE: DNA
 / ORGANISM: Chlamydia psittaci
 / US-09-738-269-56

Alignment Scores:
 Pred. No.: 1,586-121 Length: 2781
 Score: 1286.50 Matches: 327
 Percent Similarity: 47.49% Conservative: 127
 Best Local Similarity: 34.21% Mismatches: 357

Query Match: 29.95% Indels: 145
 DB: 13 Gaps: 17
 US-09-830-446-27 (1-841) x US-09-738-269-56 (1-2781)

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 Db 1 ATGAGGCGCTCTTATATATAGATTTTAAATCTGTCGACGCTGACCTTCACTTATCTTTT 60
 Qy 20 -----AsnLeuLeuIValIaIaThrThrGluLeuSerIleSerAsn 34
 Db 61 CACTTCGCAATGCAATGCAAGAGTGCCTTTACTCAAGAAATCTATCTCGATGCAAT 120
 Qy 35 SerPheArgGlyThrThrSerThrThrSerPheSerSerIleThrSerIleThrAsp 54
 Db 121 GGA-----GCATTCACCTCGCAATCTACAGACGCTCGGGA 156
 Qy 55 GlyThrAsnIleValPheLeuAspSerValIleGluAsnValProLeuThrGlyGlu 74
 Db 157 GGAACGATTTCACAGTCGAGAGTGATTTCTATGTAGATGTAGGACACAGCGGCT 216
 Qy 75 ThrGlnSerThrSerCysPheLeuAsnAspIaIaIaGlyAspLeuAsnPheLeuGly 94
 Db 217 CTGCTTCTCTCACTTTTGTTCAG-----ACTGACAGACACTTCACTTCAAGGG 267
 Qy 95 GlyGlyPheSerPheThrPheSerAsnIleAspAlaThrThrAlaSerGlyValIaIaIle 114
 Db 268 AACACACATAGCTTATCCATACAGAACGCAATGCC---GGAGCTAATCTCGCGGGAAT 324
 Qy 115 GlySerGluIaIaIaAsnIleThrValIleThrLeuSerGlyPheSerIleLeuSerPheLeu 134
 Db 325 AACGTTAACCTGCGCATAGATGATCTTACGCTGACAGATTTTCTTAAGTTGAGCTTTAAG 384
 Qy 135 LysSerProIleSerThrValIleAsnGlyLeuGlyIaIeAsnValIleGlyAsnLeu 154
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 Qy 155 SerLeuLeuAspAsnAspIleValIleuIleGlnAspAsnPheSerThrGlyAspGlyGly 174
 Db 445 AACTTAGGAATATAGCCAGATTTCTGTTTATCAGAACTATTCGCTGAGAAATGCTGA 504
 Qy 175 AlaIleAsnCys----- 178
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 Qy 178 ----- 178
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 Qy 181 SerLeuValIleAlaAsnAsnIleSerLeuSerPheIleGlyAsnSerSerThrArg 200
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Qy 241 ThrLeuSerIleSerGlyAspSerGlyAspIleIlePheGluGlyAsnThrIleGlyAla 260
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 Qy 261 -----ThrGlyThrValSerHisSerAlaIleAspLeuGlyThrSerAlaIaIaIleThr 278
 Db 1045 CAGACAAATGCTAACAATTAAGAAATGCAATTAACATTAAGCAATGTAATTTGCTC 1104
 Qy 279 AlaLeuArgAlaIaIaGlnGlyHisIleThrIleThrPheThrAspProIleThrValThrGly 298
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 Qy 299 SerThrSerValAlaAspAlaLeuAsnIleAsnSerProAspThrGlyAspAsnIleGlu 318
 Db 1165 -----AATGCTGCTGATCTTCTCACTTGTATTAAGCTGAG---GGTAT---AAAACG 1212
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 Db 1213 TATATAGAAATATATTTTTCAGAGAAAGCTCACTGAAGAACAGCTGCTGTTGGC 1272
 Qy 339 LysAsnArgThrSerIleLeuLeuGlnAsnValAlaPheLeuAsnGlyThrValIleLeu 358
 Db 1273 GATAACCTTAAGACACATTTACACAGCTATACCTTACGCTGCTGGAACCTTGTGTA 1332
 Qy 359 LysGlyAspValIleLeuSerAlaAsnGlyPheSerGlnAspAlaAsnSerIleLeuIle 378
 Db 1333 CGCAGCGGTGGAAGTAAGAAACAAACAGCTCGCAACACAGCAGATCTTTGATCTCG 1392
 Qy 379 MetAspLeuGlyThrSerLeuValAlaAsnThrGluSerIleGluLeuThrAsnLeuGlu 398
 Db 1393 ATGATGACAGGACAAAGTTATCCGCAAAAACAAAGATGCTTACACGTGACCAATCTGCT 1452
 Qy 399 IleAsnIleAspSerLeuArgAsnGlyLysLeuIleLeuLeuSerAlaIaIaThrAlaGln 418
 Db 1453 ATTAATCCGAATACTTATGATGGGAAAAAATCCCGATGATGATCCGCTGCTGCTGG 1512
 Qy 419 LysAspIleArgIleAspArgProValIleuIaIaIleSerAspGluSerPheThrGln 438
 Db 1513 AAGATGATGACTTATATGAGGTGATATGCGCTTATGATCTTACAGGGAAGTTTATGAA 1572
 Qy 439 AsnGlyPheLeuAsnGluAspHisSerThrAspGlyIleLeuGluLeuAspAlaGlyLys 458
 Db 1573 AACCATTAAGCTTAATGATACCTTAGCTTGAAGAGAAATCAACTTTCGGGAAGGTCG 1632
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 Db 1633 GTGACAAACACCAACGCGCTGATCATGCTGTGTGTGTGTGTGAACCACTATGTTAT 1692
 Qy 479 GlnGlyLysTrpThrIleAsnTrpSerThrAspAsp-----LysLys 492
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 Qy 552 ValLeuHisArgSerGlyArgGluAsnGlnArgLysPheArgHisValSerGlyGlyAla 571
 Db 1933 TTCTTCATTAAGATCGGAATGCTGAANAATGCAAAATTCGCTCATATCAGTTGGGAAT 1992
 Qy 572 ValValGlyAlaSerThrArgMetProGlyLysPheThrLeuSerLeuIlePheAlaGln 591
 Db 1993 GTGTTAGAGCCACAAACAAATCTCGAGAGAGATTTCTTATGTTGCTTCTGTCAG 2052
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[illegible]

GenCore version 5.1.6
Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus.p2n model

Run on: January 29, 2004, 10:21:11 / Search time 7888 Seconds
(without alignments)
4361.688 Million cell updates/sec

Title: US-09-830-446-27

Perfect score: 4295
Sequence: 1 MKIPRFLIBLVPTLSMSN.....FEMRGSSRSYNDAGSKIKF 841

Scoring table: BLOSUM62
Xgapop 10.0, Xgapext 0.5
Ygapop 10.0, Ygapext 0.5
Fgapop 6.0, Fgapext 7.0
Delop 6.0, Delext 7.0

Searched: 2888711 seqs, 2045481386 residues

Total number of hits satisfying chosen parameters: 5777422

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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-Q=/cgn2.1/USFTO.spool/US09830446/runat.29012004.102102.19204/app.query.fasta.1.1031
-DB=GenEmbl -Qfmt=fastap -SUFFIX=p2n.rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pcr -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pcr -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=200000000
-USER=US09830446 @CNC 1.1.5272 @runat.29012004.102102.19204 -NCPU=6 -ICPU=3
-NO_MAP -LARGEOUTERY -NEG_SCORES=0 -WAIT -DSFLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database : GenEmbl :
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20: em_om :
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23: em_pac :
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25: em_pl :
26: em_ro :
27: em_sbs :
28: em_un :

29: em_vl :
30: em_hcg_hum :
31: em_hcg_inv :
32: em_hcg_other :
33: em_hcg_mus :
34: em_hcg_pin :
35: em_hcg_rtd :
36: em_hcg_mam :
37: em_hcg_vrt :
38: em_ay :
39: em_hcgo_hum :
40: em_hcgo_mus :
41: em_hcgo_other :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	4295	100.0	2526	6 AX349617	AX349617 Sequence
2	4295	100.0	10574	1 AE001586	AE001586 Chlamydia
3	4295	100.0	12127	1 AE002235	AE002235 Chlamydia
4	4295	100.0	26920	1 CPN133035	AJ133035 Chlamydia
5	4278	99.6	2526	6 AB1813	AB1813 Sequence 7
6	4260	99.2	299650	1 AP002545	AP002545 Chlamydia
7	4255	99.1	110000	6 AR310754_00	AR310754 Sequence 29
8	2603	60.6	1830	6 AB1855	AB1855 Sequence 9
9	1569.5	36.5	2787	6 AB1835	AB1835 Sequence 9
10	1558.5	36.3	16448	1 AE001587	AE001587 Chlamydia
11	1497	34.9	2520	6 AX662085	AX662085 Sequence
12	1487	34.9	2520	6 AX66157	AX66157 Sequence
13	1487	34.9	6110	1 CP065942	U65942 Chlamydia
14	1487	34.9	6234	1 CP065943	U65943 Chlamydia
15	1435.5	33.4	2787	6 AX349593	AX349593 Sequence
16	1435.5	33.4	3200	6 AB1827	AB1827 Sequence 1
17	1435.5	33.4	6030	1 CP0654	AJ001311 Chlamydia
18	1435.5	33.4	10757	1 AE001628	AE001628 Chlamydia
19	1435.5	33.4	12676	1 AE002192	AE002192 Chlamydia
20	1435.5	33.4	17280	1 CPN133034	AJ133034 Chlamydia
21	1435.5	33.4	110000	6 AR310754_05	Continuation (6 of
22	1435.5	33.4	30650	1 AP002546	AP002546 Chlamydia
23	1415.5	33.0	2793	6 AX349523	AX349523 Sequence
24	1415.5	33.0	10026	1 AE002193	AE002193 Chlamydia
25	1415.5	33.0	15068	1 AE001627	AE001627 Chlamydia
26	1407.5	32.8	2787	6 AX349573	AX349573 Sequence
27	1406.5	32.7	2793	6 AB1841	AB1841 Sequence 15
28	1406.5	32.7	2815	6 AB1829	AB1829 Sequence 3
29	1406.5	32.7	12676	1 AE002192	AE002192 Chlamydia
30	1406.5	32.7	17280	1 CPN133034	AJ133034 Chlamydia
31	1406.5	32.7	30650	1 AP002546	AP002546 Chlamydia
32	1402.5	32.7	2757	6 AB1837	AB1837 Sequence 11
33	1396	32.5	300955	1 AE016996	AE016996 Chlamydia
34	1390	32.1	10757	1 AE001628	AE001628 Chlamydia
35	1379.5	32.1	2787	6 AX349511	AX349511 Sequence
36	1377.5	32.1	2787	6 AB1839	AB1839 Sequence 13
37	1366.5	31.8	300512	1 AE016995	AE016995 Chlamydia
38	1365	31.8	110000	6 AR310754_05	Continuation (6 of
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42	1335.5	31.1	2811	6 AX349631	AX349631 Sequence
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RESULT 1

ALIGNMENTS

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LOCUS         Sequence 140 from Patent WO0202606.
DEFINITION   AX349617
ACCESSION    AX349617.1 GI:18615415
VERSION      AX349617.1
KEYWORDS     Chlamydia pneumoniae
SOURCE       Chlamydia pneumoniae
ORGANISM     Bacteria; Chlamydiae; Chlamydiaceae; Chlamydia.
REFERENCE    1 Ratti, G. and Grandi, G.
AUTHORS      Immunisation against Chlamydia pneumoniae
TITLE        Patent: WO 0202606-A 140 10-JAN-2002;
JOURNAL      Chiron S.P.A. (IT)
FEATURES     source
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             /organism="Chlamydia pneumoniae"
             /mol_type="genomic DNA"
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 AUTHORS Kalman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Olinger, L.,
 Olinger, L., Grimwood, J., Davis, R.W. and Stephens, R.S.
 TITLE Comparative genomes of Chlamydia pneumoniae and C. trachomatis
 JOURNAL Nat. Genet. 21 (4), 385-389 (1999).

MEDLINE 9920606
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 Grimwood, J., Davis, R.W. and Stephens, R.S.
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 JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University
 of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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Percent Similarity: 100.00% Conservative: 0
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US-09-830-446-27 (1-841) x AB002235 (1-12127)

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 ORGANISM
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 REFERENCES
 1. Daugaard, L., Hjerno, K., Knudsen, K., Madsen, A.S., Christiansen, G.
 and Birkelund, S.
 Unpublished
 2 (bases 1 to 26920)
 JOURNAL
 Boesen, T.
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US-09-830-446-27 (1-841) x CPN133035 (1-26920)

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 AUTHORS Maden A. and Birkelund S.
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 AUTHORS
 1 Shirai, M., Hirakawa, H., Uchi, K., Tabuchi, M., Kishi, F., Kimoto, M.,
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 Matsushima, H., Tanaka, C., Furukawa, S., Miura, K., Nakazawa, A.,
 Ishii, K., Shiba, T., Hattori, M., Kuwara, S. and Nakazawa, T.
 Comparison of outer membrane protein genes omp and pmp in the whole
 genome sequences of Chlamydia pneumoniae isolates from Japan and
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 J. Infect. Dis. 181 Suppl 3, S524-S527 (2000)
 JOURNAL
 MEDLINE
 PUBMED
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 Shirai, M.
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 Submitted (04-JUL-2000) Mutsunori Shirai, Yamaguchi University
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 Minamikogushi, Ube, Yamaguchi 755-8505, Japan
 (E-mail: mshirai@po.cc.yamaguchi-u.ac.jp, Tel: 81-836-22-2227,
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SOURCE Unknown.
ORGANISM Unknown.
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REFERENCE 1 (bases 1 to 1230025)
AUTHORS Griffiths,R., Hoijsch,S.K., Zagursky,R.J., Metcalfe,B.J., Peek,J.A.,
Sankaran,B. and Fletcher,L.D.
TITLE Chlamydia pneumoniae polymucleotides and uses thereof
JOURNAL Patent: US 6559294-A 1 06-MAY-2003;
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ACCESSION AB1835
VERSION AB1835.1 GI:6731868
KEYWORDS
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ORGANISM unidentified
REFERENCE 1 (bases 1 to 2787)
AUTHORS Madsen, A. and Birke Lund, S.
TITLE NOVEL SURFACE EXPOSED PROTEINS FROM CHLAMYDIA PNEUMONIAE
JOURNAL Patent: WO 9858953-A 9 30-DEC-1998;
MADSEN ANNA SØRIB (DK); BIRKE LUND SVEND (DK)
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 Kaiman, S., Mitchell, W., Marathe, R., Lammel, C., Fan, J., Hyman, R. W., Olinger, L., Grimwood, J., Davis, R. W. and Stephens, R. S. Comparative genomes of Chlamydia pneumoniae and C. trachomatis Nat. Genet. 21 (4), 385-389 (1999)
 JOURNAL Submitted (01-DEC-1998) Program in Infectious Diseases, University of California, 235 Earl Warren Hall, Berkeley, CA 94720, USA
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Db	616	TTGAGTTTGAC-AAAAATGTCAGTTTGCTCTTCAGCAAAAACCTTTCAACGGATATAGC		674
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QY	178	-----		178
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QY	215	GLYGLUTHRLEUPE-----GLINGLYASNTTHRALPROTHRALALAEGLY		229
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QY	427	ValValleuAlaIleSerAspGluSerPheTyGlnAsnGlyPheLeuAsnGluAspHis	446
DB	1734	ATCACTTATTATGACCCGACGGACGGCTTTATGAAATCATAGTTTAAGAAATCTCCAG	1793
QY	447	SerTybAspGlyIleLeuGlnLeuAspAlaGlyLybAspIleValIleSerAla--AspS	466
DB	1794	TCCATACGC--ACCTTAGAGCTCAAGAGCTTGGAACTGTGAACGTGAACAGCACCGACGTACT	1855
QY	466	erArgSerIleAspAlaValGlnSerPro-TyrGlyTyrglnGlyLeuTyb--ThrIle	484
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QY	485	AsnTrpSerThrAsp--AspLybLeuAlaThrValSerTrpAlaTybGlnSerPheAsn	503
DB	1911	GTTTGGGGGACAGGGGGCTTACAGACGTGCACCTTCACTGAGACTAATAACGGCATATT	1976
QY	504	ProThrAlaGlnGlnGluAlaProLeuValProAsnLeuLeuTrpGlySerPheIleAsp	523
DB	1971	CCTAATCCCGACGTATCGGCTCTTATAGTCCCTAATAGCTTATAGTGAATTAATATAT	2036
QY	524	ValArgSerPheGlnAsnPheIleGlnLeuGlyThrGlnGlyAlaProTybGluLybArg	543
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QY	564	PheArgHisValSerGlyGlyAlaValValGlyAlaSerThrArgMetProGlyGlyAsp	583
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QY	584	ThrLeuSerLeuGlyPheAlaGlnLeuPheAlaArgAspLybAspTybPheMetAsnThr	603
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QY	624	ValValSerIleLeuLeuGlyGlyGlyLeuArgGlnIleLeuLeuProTybValSer	643
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QY	644	LybThrLeuProCysSerPheTybGlyGlnLeuSerTybGlyHisThrAspHisArgMet	663
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QY	664	LybThrGlnSerLeuProProProProThrLeuSerThrAspHisThrSerTrpGly	683
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QY	684	GlyTybValTrpAlaGlyGlnLeuGlyThrArg-----ValAlaValGluAsnThrSer	701
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QY	722	GlnAspSerPheValGlnLeuGlyAlaIleSerArgAspPheSerAspSerHisLeuTyb	741
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Db      2649 AATCTGCCTTACCTACCGGATCCGATTTGATAGGAATCAAGCTGCAAGATGCAAGC 2708
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Qy      800 GlyTLeValGlnAlaSerGlyPheArgSerLeuGlyValAlaAlaGluLeuPheGlyAsn 819
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DEFINITION AX662085
VERSION    AX662085.1 GI:29163040
KEYWORDS
SOURCE     Chlamydomophila peitraci
ORGANISM   Bacteria; Chlamydiales; Chlamydiaceae; Chlamydomophila.
REFERENCE  1 Johnston,S.A., Stenke-Hale,K., Sykes,K.F. and Kaltenboeck,B.
AUTHORS    Methods and compositions for vaccination comprising nucleic acid
TITLE       and/or polypeptide sequences of chlamydia peitraci
JOURNAL     Patent: WO 02053588-A 22-11-JUL-2002;
            BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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ORIGIN

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Alignment Scores:

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Percent Similarity: 56.21% Conservative: 132
Best Local Similarity: 41.03% Mismatches: 321
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US-09-830-446-27 (1-841) x AX662085 (1-2520)

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Qy      39 ThrThrSerThrThrSerPheSerSerLysThrSerSerAlaThrAspGlyThrAsnTyr 58
Db      115 AATGTAACCTCTGAAGAGTTCCAGGTAAAGAACTTCATCA-----GGAACACGTAAT 168
Qy      59 ValPheLysAspSerValValIleGluAsnValProLysThrGlyLysThrGlnSerThr 78
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Qy      99 PheThrPheSerAsnIleAspAlaThrThrAlaSerGlyValAlaAlaIleGlySerGlnAla 118
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Qy      119 AlaAsnLysThrValThrLeuSerGlyPheSerAlaLeuSerPheLeuLysSerProAla 138
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Qy      139 SerThrValThrAsnGlyLeuGlyValAlaIleAsnValLysGlyAsnLeuSerLeuAsp 158
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Qy      349 ValAlaPheLysAsnGlyThrValValLeuLysGlyAspValValLeuSerAlaAsnGly 368
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Qy      369 PheSerGlnAspAlaAsnSerLysLeuIleMetAspLeuGlyThrSerLeu----- 385
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Qy      483 ThrIleAapTyrSerThrAap-----AaplyblybAlaThrValSerTyrAlaGln 500
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Qy      521 PheIleAapValArgSerPheGlnAapPheIleGlnLeuGlyThrGlnGlyAlaProTyr 540
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Qy      541 GlnlybArgPheTyrValAlaGlylleSerAapValLeuHieArgSerGlyArgGln 560
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Qy      661 HieArgMetIlybThrGln-----SerLeuProProProProThrLeuSerThr 677
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Qy      757 GlnGln-----TyrTyrHieValAlaIleMetIlybSerProAapValCysArgSer 773
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Qy      812 AlaAlaAlaGlnLeuPheGlyAapPheGlyPheGlnIlybThrArgGlySerSerArgTyr 831
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AX666157
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DEFINITION Sequence 22 from Patent WO247718.
ACCESSION AX666157
VERSION AX666157.1 GI:29290977
KEYWORDS
SOURCE
ORGANISM Chlamydomonas reinhardtii
REFERENCE 1
AUTHORS Johnson, S.A.
TITLES Methods and compositions for vaccination comprising nucleic acid
JOURNAL ad/or polypeptide sequences of 1(chlamydia)
BOARD OF REGENTS THE UNIVERSITY OF TEXAS SYSTEM (US)
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Percent Similarity: 56.21% Conservative: 132
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 VERSION U65942.1 GI:1617505
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 SOURCE Chlamydia abortus
 ORGANISM Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydia.
 REFERENCE 1 (sites)
 Longbottom, D., Russell, M., Jones, G.B., Iainson, F.A. and
 Herring, A.J.
 Identification of a multigene family coding for the 90 kDa proteins
 of the ovine abortion subtype of Chlamydia psittaci
 JOURNAL PEMS Microbiol. Lett. 142 (2-3), 277-281 (1996)
 MEDLINE 96406378
 PUBMED 8810511
 REFERENCE 2 (sites)
 Longbottom, D., Russell, M., Dunbar, S.M., Jones, G.B. and Herring, A.J.
 Molecular cloning and characterization of the genes coding for the
 highly immunogenic cluster of 90-kilodalton envelope proteins from
 the Chlamydia psittaci subtype that causes abortion in sheep
 infect. Immun. 66 (4), 1317-1324 (1998)
 JOURNAL 98187897
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 REFERENCE 3 (bases 1 to 6110)
 Longbottom, D.
 Direct Submission
 Submitted (02-AUG-1996) Moredun Research Institute, International
 Research Centre, Pentlands Science Park, Bush Loan, Pentlands,
 Midlothian EH26 0PZ, UK
 JOURNAL
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US-09-830-446-27 (1-841) x CPU65942 (1-6110)

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precursor, genes, complete cds.
U65943
U65943.1 GI:1617508

ACCESSION
VERSION
KEYWORDS

SOURCE
ORGANISM
Chlamydomophila abortus
Chlamydomophila abortus
Bacteria; Chlamydiae; Chlamydiales; Chlamydiaceae; Chlamydomophila.
1 (sites)

REFERENCE
AUTHORS
Longbottom,D., Russell,M., Jones,G.R., Lainson,F.A. and
Herring,A.J.
Identification of a multigene family coding for the 90 kDa proteinase
of the ovine abortion subtype of Chlamydia psittaci
FEMS Microbiol. Lett. 142 (2-3), 277-281 (1996)

JOURNAL
MEDLINE
PUBMED
96406378
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REFERENCE
AUTHORS
Longbottom,D., Russell,M., Dunbar,S.M., Jones,G.R. and Herring,A.J.
Molecular cloning and characterization of the genes coding for the
highly immunogenic cluster of 90-kilodalton envelope proteins from
the Chlamydia psittaci subtype that causes abortion in sheep
Infect. Immun. 66 (4), 1317-1324 (1998)

JOURNAL
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REFERENCE
AUTHORS
Longbottom,D.
Direct Submission
Submitted (02-AUG-1996) Moreduin Research Institute, International
Research Centre, Pentlands Science Park, Bush Loan, Pentcuk,
Midlothian EH26 0PZ, UK
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ACCESSION  AX349593
VERSION    AX349593.1 GI:18615403
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ORGANISM    Chlamydomonas pneumoniae
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REFERENCE 1
AUTHORS    Ratti, G. and Grandi, G.
TITLE      Immunisation against Chlamydia pneumoniae
JOURNAL    Patent: WO 0202606-A 116 10-JAN-2002;
          Chiron S.p.A. (IT)
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LOCATION/Qualifiers
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Listing first 45 summaries

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36	341	7.9	2103	4	US-09-620-412C-344	Sequence 344, App
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38	333	7.8	2076	4	US-09-620-412C-312	Sequence 312, App
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44	266	6.2	1965	4	US-09-620-412C-356	Sequence 356, App
45	266	6.2	2052	4	US-09-598-419-356	Sequence 356, App

ALIGNMENTS

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RESULT 1
US-09-198-452A-1
; Sequence 1, Application US/09198452A
; Patent No. 6559294
;
GENERAL INFORMATION:
; APPLICANT: Griffiths, R.
; TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragment thereof and uses thereof, in particular for the diagnosis, prevention and treatment of infection
; FILE REFERENCE: 9710-003-999
; CURRENT APPLICATION NUMBER: US/09/198,452A
; CURRENT FILING DATE: 1998-11-24
; NUMBER OF SEQ ID NOS: 6849
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ORGANISM: Chlamydia pneumoniae
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Alignment Scores:

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Score:	4255.00	Matches:	840
Percent Similarity:	99.76%	Conservative:	0
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Query Match:	99.07%	Indels:	2
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Db	29010	TTATTAGAGGTGGTACTACCGAAGAAATTAATCGGCTAAGCAATAGCTTCGATGGAACTTAA	29065
QY	41	SetThrThrSerPheSerSerIlyThrSerSerAlaThrAspGlyThrAenValPhe	60
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Dh	29789	CGTGTCTCGAAGGACATACGATATATCTTTATGATCCGATTCCTGTAAACAGATCGACA	29848
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RESULT 2

US-09-198-452A-1/c

Sequence 1, Application US/09198452A

Patent No. 6559294

GENERAL INFORMATION:

APPLICANT: Griffiths, R.

TITLE OF INVENTION: Chlamydia pneumoniae genomic sequence and polypeptides, fragments

TITLE OF INVENTION: Therect and uses thereof, in particular for the diagnosis, prevention

FILE REFERENCE: 9710-003-999

CURRENT APPLICATION NUMBER: US/09/198,452A

NUMBER OF SEQ ID NOS: 6849

SEQ ID NO 1

LENGTH: 1230025

Jan 30

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